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(12) **United States Patent**
**Smolke et al.**

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(54) **COMPOSITIONS AND METHODS FOR PRODUCING BENZYLISOQUINOLINE ALKALOIDS**


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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

This patent is subject to a terminal disclaimer.


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(51) **Int. Cl.**

| | |
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| ***C12N 1/20*** | (2006.01) |
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| ***C12N 15/00*** | (2006.01) |
| ***C12N 9/02*** | (2006.01) |
| ***C12N 9/14*** | (2006.01) |
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| ***C12N 9/88*** | (2006.01) |
| ***C12N 9/10*** | (2006.01) |
| ***C12N 15/81*** | (2006.01) |
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| ***C12P 13/00*** | (2006.01) |
| ***C12P 17/18*** | (2006.01) |

(52) **U.S. Cl.**

CPC ............... ***C12P 17/12*** (2013.01); ***C12N 9/0022*** (2013.01); ***C12N 9/0059*** (2013.01); ***C12N 9/1007*** (2013.01); ***C12N 9/1096*** (2013.01); ***C12N 9/88*** (2013.01); ***C12N 15/81*** (2013.01); ***C12P 7/24*** (2013.01); ***C12P 13/001*** (2013.01); ***C12P 17/182*** (2013.01)

(58) **Field of Classification Search**

CPC .... C12N 15/81; C12N 9/1007; C12N 9/0022; C12N 9/0059; C12N 9/88; C12N 9/1096; C12P 7/12

See application file for complete search history.


(56) **References Cited**


U.S. PATENT DOCUMENTS

| | | | |
|---|---|---|---|
| 7,193,127 | B1 | 3/2007 | Kutchan et al. |
| 7,390,642 | B2 | 6/2008 | Kutchan et al. |
| 2005/0106588 | A1 | 5/2005 | Kutchan et al. |
| 2005/0139490 | A1 | 6/2005 | Chou et al. |
| 2007/0199090 | A1 | 8/2007 | Apuya et al. |
| 2008/0176754 | A1 | 7/2008 | Smolke et al. |
| 2014/0273109 | A1 | 9/2014 | Smolke et al. |

FOREIGN PATENT DOCUMENTS

| | | | |
|---|---|---|---|
| EP | 1512748 | A1 | 3/2005 |
| EP | 1837396 | A1 | 9/2007 |
| WO | WO 2008/067070 | A2 | 6/2008 |
| WO | WO 2011/058446 | A2 | 5/2011 |
| WO | WO 2014/143744 | A2 | 9/2014 |
| WO | WO 2015/066642 | A1 | 5/2015 |

OTHER PUBLICATIONS

Branden et al. Introduction to Protein Structure, Garland Publishing Inc., New York, p. 247, 1991.*

Cooper et al., "On the amine oxidases of *Klebsiella aerogenes* strain W70," *FEMS Microbiol. Lett.*, 146(1):85-89 (1997).

Facchini et al., "Differential and Tissue-Specific Expression of a Gene Family for Tyrosine/Dopa Decarboxylase in Opium Poppy," *J. Biol. Chem.*, 269(43):26684-26690 (1994).

Hiroi et al., "Dopamine Formation from Tyramine by CYP2D6," *Biochemical & Biophysical Research Communications*, 249:838-843 (1998).

Iraqui et al., "Characterisation of *Saccharomyces cerevisiae* AR08 and AR09 genes encoding aromatic aminotransferases I and II reveals a new aminotransferase subfamily," *Mol. Gen. Genet.*, 257(2):238-248 (1998).

Kutchan et al., "Molecular Genetics of Plant Alkaloid Biosynthesis," *Alkaloids*, 50:257-316 (1998).

Kutchan, T.M., "Heterologous Expression of Alkaloid Biosynthetic Genes . . . A Review," *Gene*, 179(1):73-81 (1996).

Moerner et al., "Illuminating single molecules in condensed matter," *Science*, 283(5408):1670-1676 (1999).

Ounaroon et al., "(*R,S*)-Reticuline 7-*0*-methyltransferase and (*R,S*)-norcoclaurine 6-*0*-methyltransferase of *Papaver somniferum*—cDNA cloning and characterization of methyl transfer enzymes of alkaloid biosynthesis in opium poppy," *Plant J.*, 36(6):808-819 (2003).


(Continued)

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(74) *Attorney, Agent, or Firm* — Wilson Sonsini Goodrich Rosati

(57) **ABSTRACT**


The present invention relates to host cells that produce compounds that are characterized as benzylisoquinolines, as well as select precursors and intermediates thereof. The host cells comprise one, two or more heterologous coding sequences wherein each of the heterologous coding sequences encodes an enzyme involved in the metabolic pathway of a benzylisoquinoline, or its precursors or intermediates from a starting compound. The invention also relates to methods of producing the benzylisoquinoline, as well as select precursors and intermediates thereof by culturing the host cells under culture conditions that promote expression of the enzymes that produce the benzylisoquinoline or precursors or intermediates thereof.


**18 Claims, 30 Drawing Sheets**

(56) **References Cited**

OTHER PUBLICATIONS

Samanani et al., "Molecular cloning and characterization of norcoclaurine synthase, an enzyme catalyzing the first committed step in benzylisoquinoline alkaloid biosynthesis," *Plant J.*, 40(2):302-313 (2004).
Stewart et al., "A Chemist's Perspective on the Use of Genetically Engineered Microbes as Reagents for Organic Synthesis," *Biotechnology and Genetic Engineering Reviews* 14:67-143 (1997).
Vuralhan et al., "Identification and characterization of phenylpyruvate decarboxylase genes in *Saccharomyces cerevisiae,*" *Appl. Environ. Microbiol.*, 69(8):4534-4541 (2003).
Zenk et al., "Benzylisoquinoline Biosynthesis by Cultivated Plant Cells and Isolated Enzymes," *Journal of Natural Products*, 48,(5):725-738 (1985).
Single Molecule Detection and Manipulation Workshop. Apr. 17-18, 2000. Retrieved from http://www.nigms.nih.gov/news/reports/single_molecules.html.
International Search Report for PCT/US07/81974, mailed Jul. 8, 2008.
Allen et al., "RNAi-Mediated Replacement of Morphine with the Nonnarcotic Alkaloid Reticuline in Opium Poppy", Nat. Biotechnol. (2004), 22:1559-1566.
Backes et al., "Organization of Multiple Cytochrome P450s with NADPH-Cytochrome P450 Reductase in Membranes", Pharmacol. Ther. (2003), 98:221-233.
Bayer et al., "Synthesis of Methyl Halides from Biomass Using Engineered Microbes", J. Am. Chem. Soc. (2009), 131:6508-6515.
Bruce et al., "Microbial Degradation of the Morphine Alkaloids. Purification and Characterization of Morphine Dehydrogenase from Pseudomonas putida M10", Biochem. J. (1991), 274(3):875-880.
Choi et al., "Molecular Cloning and Characterization of Coclaurine N-Methyltransferase from Cultured Cells of Coptis japonica", J. Biol. Chem. (2002), 277:830-835.
Dumas et al., "11 Beta-Hydroxylase Activity in Recombinant Yeast Mitochondria. In vivo Conversion of 11-Deoxycortisol to Hydrocortisone", Eur. J. Biochem. (1996), 238:495-504.
Fisinger et al., "Thebaine Synthase: a New Enzyme in the Morphine Pathway in Papaver somniferum", Natural Product Communications (2007), 2(3):249-253.
French et al., "Biological Production of Semisynthetic Opiates Using Genetically Engineered Bacteria", Biotechnology (N Y) (1995), 13:674-676.
Geissler et al., "Molecular Modeling and Site-Directed Mutagenesis Reveal the Benzylisoquinoline Binding Site of the Short-Chain Dehydrogenase/Reductase Salutaridine Reductase", Plant Physiol. (2007), 143(4):1493-503.
Grothe et al., "Molecular Characterization of the Salutaridinol 7-0-Acetyltransferase Involved in Morphine Biosynthesis in Opium Poppy Papaver somniferum", J. Biol. Chem. (2001), 276:30717-30723.
Hagel et al., "Benzylisoquinoline Alkaloid Metabolism: a Century of Discovery and a Brave New World", Plant Cell Physiol. (2013), 54:647-672.
Hawkins et al., "Production of Benzylisoquinoline Alkaloids in Saccharomyces Cerevisiae", Nature Chemical Biology (2008), 4:564-573.
Ikezawa et al., "Molecular Cloning and Characterization of CYP719, a Methylenedioxy Bridge-Forming Enzyme that Belongs to a Novel P450 Family, from Cultured Coptis japonica Cells", J. Biol. Chem. (2003), 278:38557-38565.
Ikezawa et al., "Molecular Cloning and Characterization of Methylenedioxy Bridge-Forming Enzymes Involved in Stylopine Biosynthesis in Eschscholzia californica", FEBS J. (2007), 274:1019-1035.
International search report and written opinion dated Sep. 15, 2015 for PCT Application No. PCT/US2014/027833 (with publication).
Jensen et al., "Plant NADPH-Cytochrome P450 Oxidoreductases", Phytochemistry (2010). 71:132-141.
Kushnirov, "Rapid and Reliable Protein Extraction from Yeast", Yeast (2000), 16:857-860.
Larkin et al., "Increasing Morphinan Alkaloid Production by Over-Expressing Codeinone Reductase in Transgenic Papaver somniferum", Plant Biotechnol. J. (2007), 5:26-37.
Lenz et al., "Acetyl Coenzyme A: Salutaridinol-7-O Acetyltransferase from Papaver somniferum Plant Cell Cultures", J. Biol. Chem. (1995), 270:31091-31096.
Lenz et al., "Purification and Properties of Codeinone Reductase (NADPH) from Papaver somniferum Cell Cultures and Differentiated Plants", Eur. J. Biochem. (1995), 233:132-139.
Morishige et al., "Molecular Characterization of the Sadenosyl-L-Methionine:3'-Hydroxy-N-Methylcoclaurine 4'O-Methyltransferase Involved in Isoquinoline Alkaloid Biosynthesis in Coptis japonica", J. Biol. Chem. (2000), 275:23398-23405.
Notice of allowance dated Nov. 7, 2014 for U.S. Appl. No. 11/875,814.
Office action dated Feb. 18, 2009 for U.S. Appl. No. 11/875,814.
Office action dated Dec. 29, 2009 for U.S. Appl. No. 11/875,814.
Office action dated Dec. 3, 2013 for U.S. Appl. No. 11/875,814.
Office action dated May 23, 2014 for U.S. Appl. No. 11/875,814.
Office action dated Dec. 10, 2015 for U.S. Appl. No. 14/211,611.
Sandig et al., "Regulation of Endoplasm ic Reticulum Biogenesis in Response to Cytochrome P450 Overproduction", Drug Metab. Rev. (1999), 31:393-410.
Sato et al., "Purification and Characterization of S-adenosyl-L-methionine: norcoclaurine 6-0-methyltransferase from Cultured Coptis japonica Cells", Eur. J. Biochem. (1994), 225:125-131.
Siddiqui et al., "Advancing Secondary Metabolite Biosynthesis in Yeast with Synthetic Biology Tools", FEMS Yeast Res. (2012), 12:144-170.
Unterlinner et al., "Molecular Cloning and Functional Expression of Codeinone Reductase: the Penultimate Enzyme in Morphine Biosynthesis in the Opium Poppy Papaver somniferum", Plant J. (1999), 18:465-475.
Zhang et al., "14-Hydroxylation of Opiates: Catalytic Direct Autoxidation of Codeinone to 14-Hydroxycodeinone", J. Am. Chem. Soc. (2005), 127:7286-7287.
Ziegler et al., "Removal of Substrate Inhibition and Increase in Maximal Velocity in the Short Chain Dehydrogenase/Reductase Salutaridine Reductase Involved in Morphine Biosynthesis", J. Biol. Chem. (2009), 284:26758-26767.
Zimmer et al., "Protein Quality—a Determinant of the Intracellular Fate of Membrane-Bound Cytochromes P450 in Yeast", DNA Cell Biol. (1997), 16:501-514.

* cited by examiner

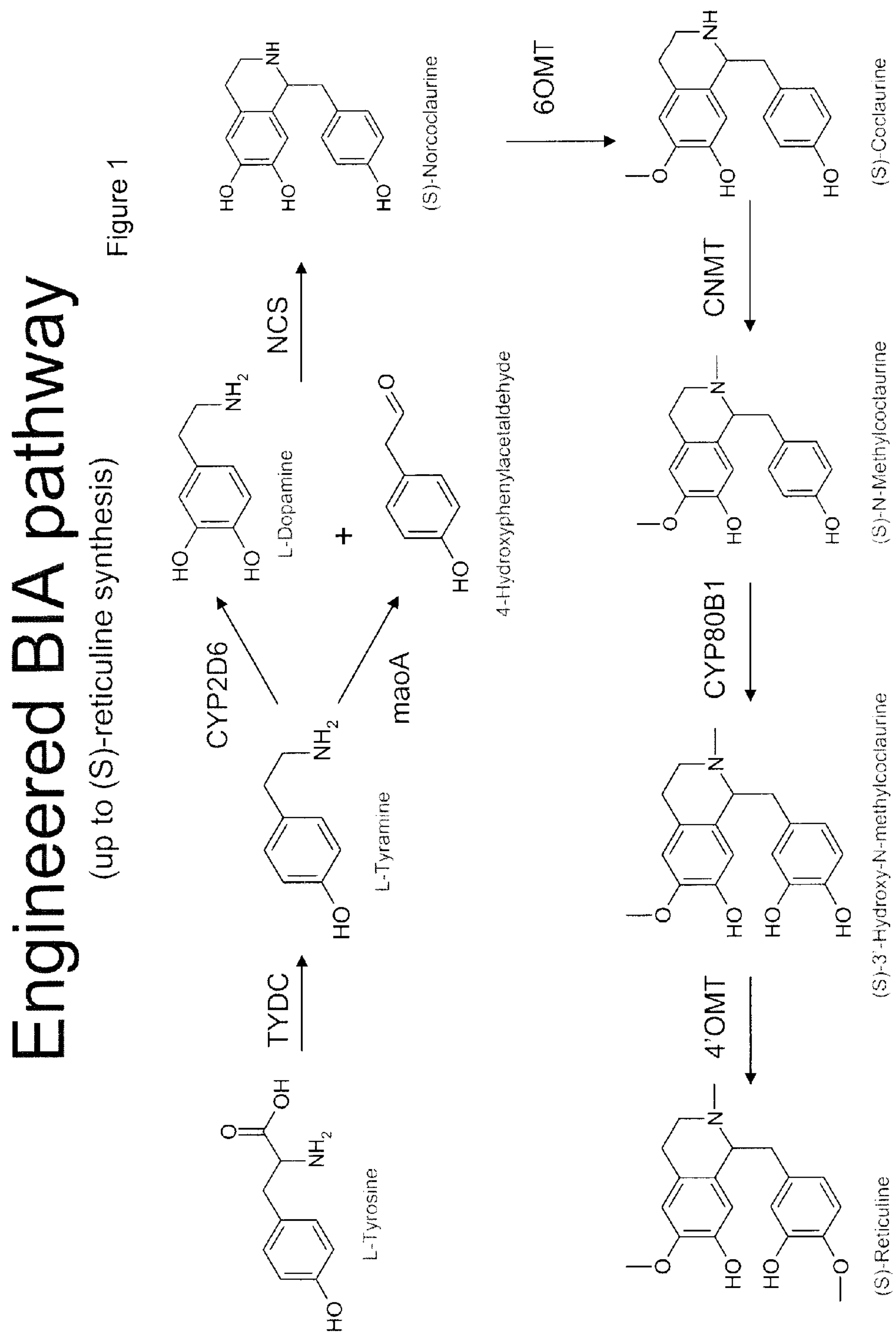

Engineered BIA pathway
(up to (S)-reticuline synthesis)
Figure 1
L-Tyrosine
TYDC
L-Tyramine
CYP2D6
maoA
L-Dopamine
4-Hydroxyphenylacetaldehyde
NCS
(S)-Norcoclaurine
6OMT
(S)-Coclaurine
CNMT
(S)-N-Methylcoclaurine
CYP80B1
(S)-3'-Hydroxy-N-methylcoclaurine
4'OMT
(S)-Reticuline

FIG. 1

Dopamine production

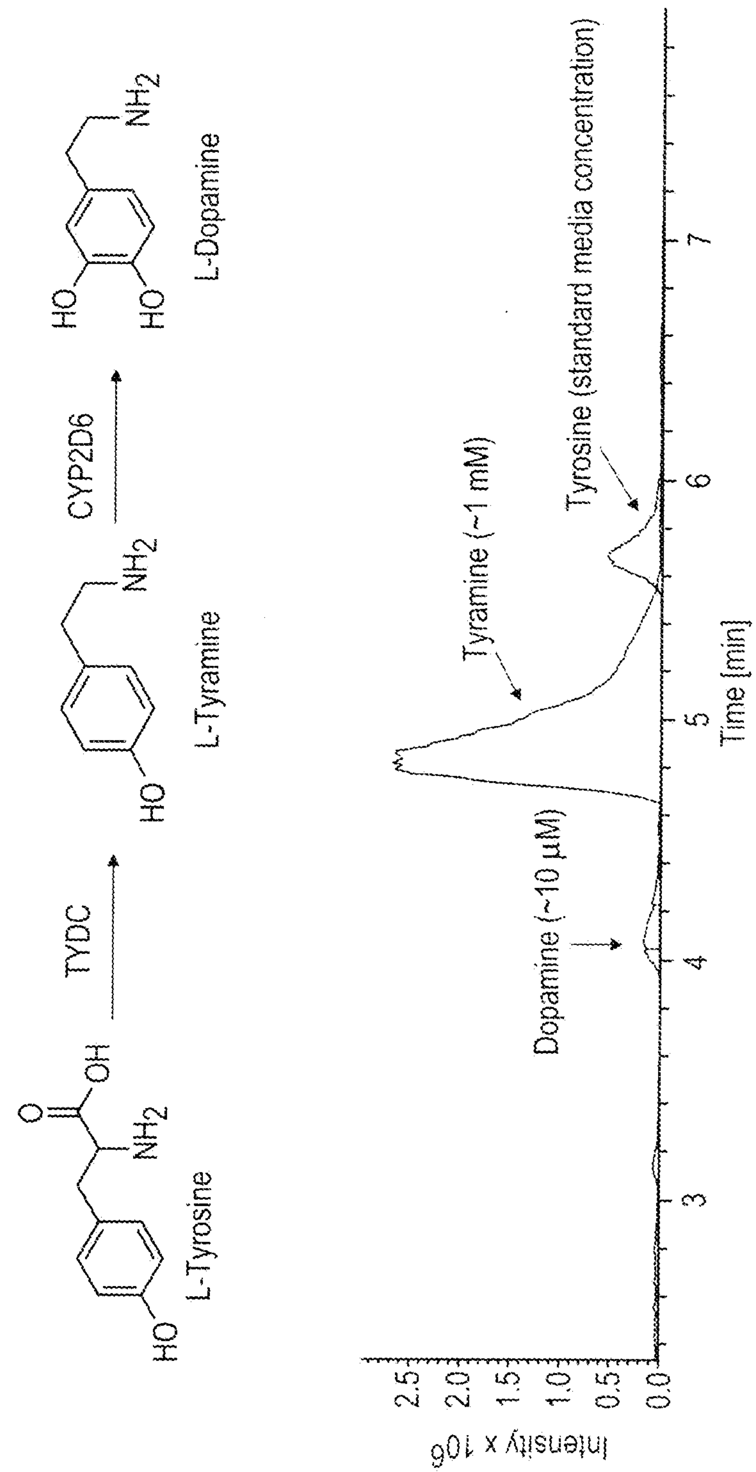



FIG. 2

# Alternatives for 4-HPA production

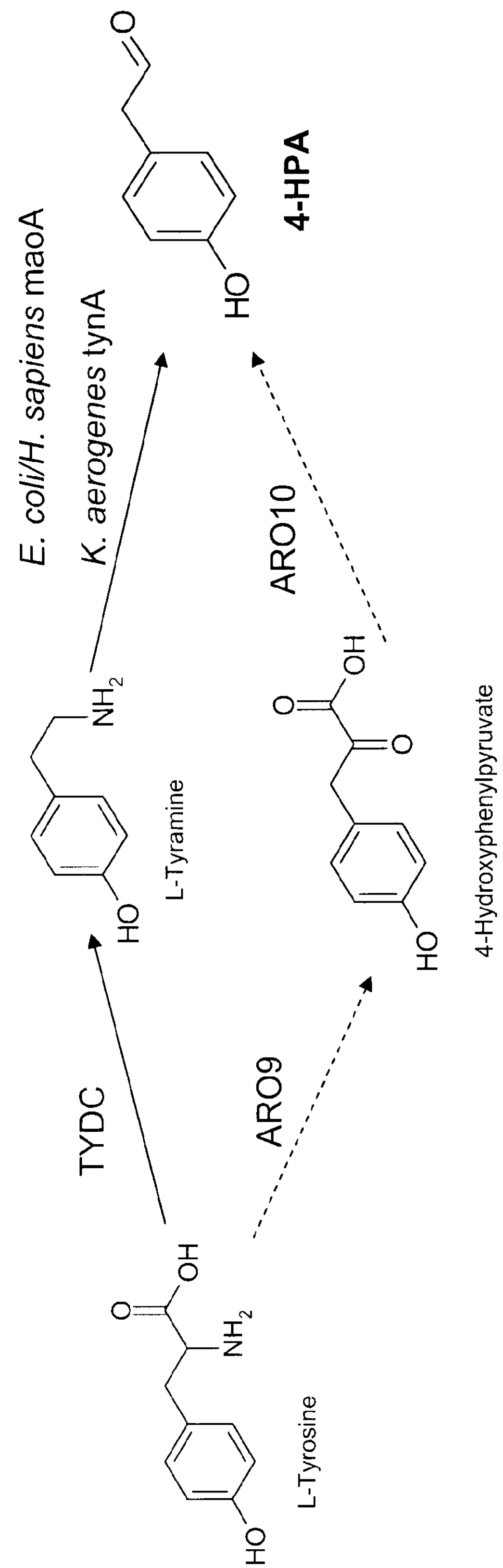



FIG. 3

Norcoclaurine synthase (NCS) activity

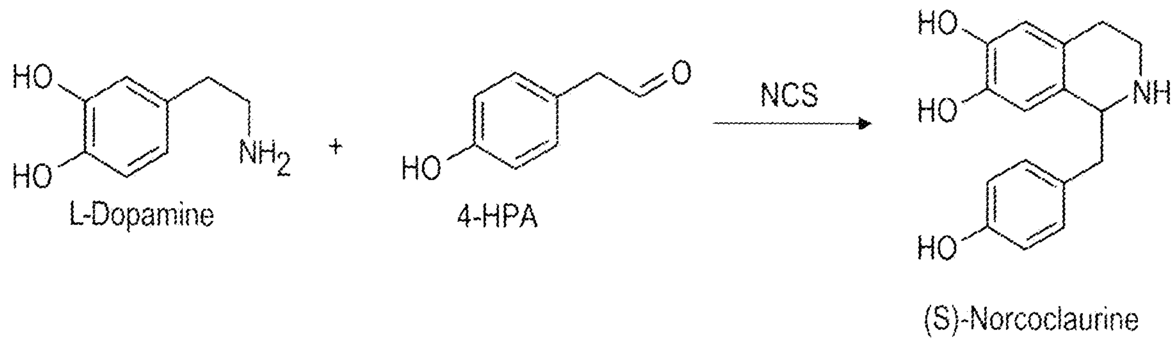



FIG. 4A

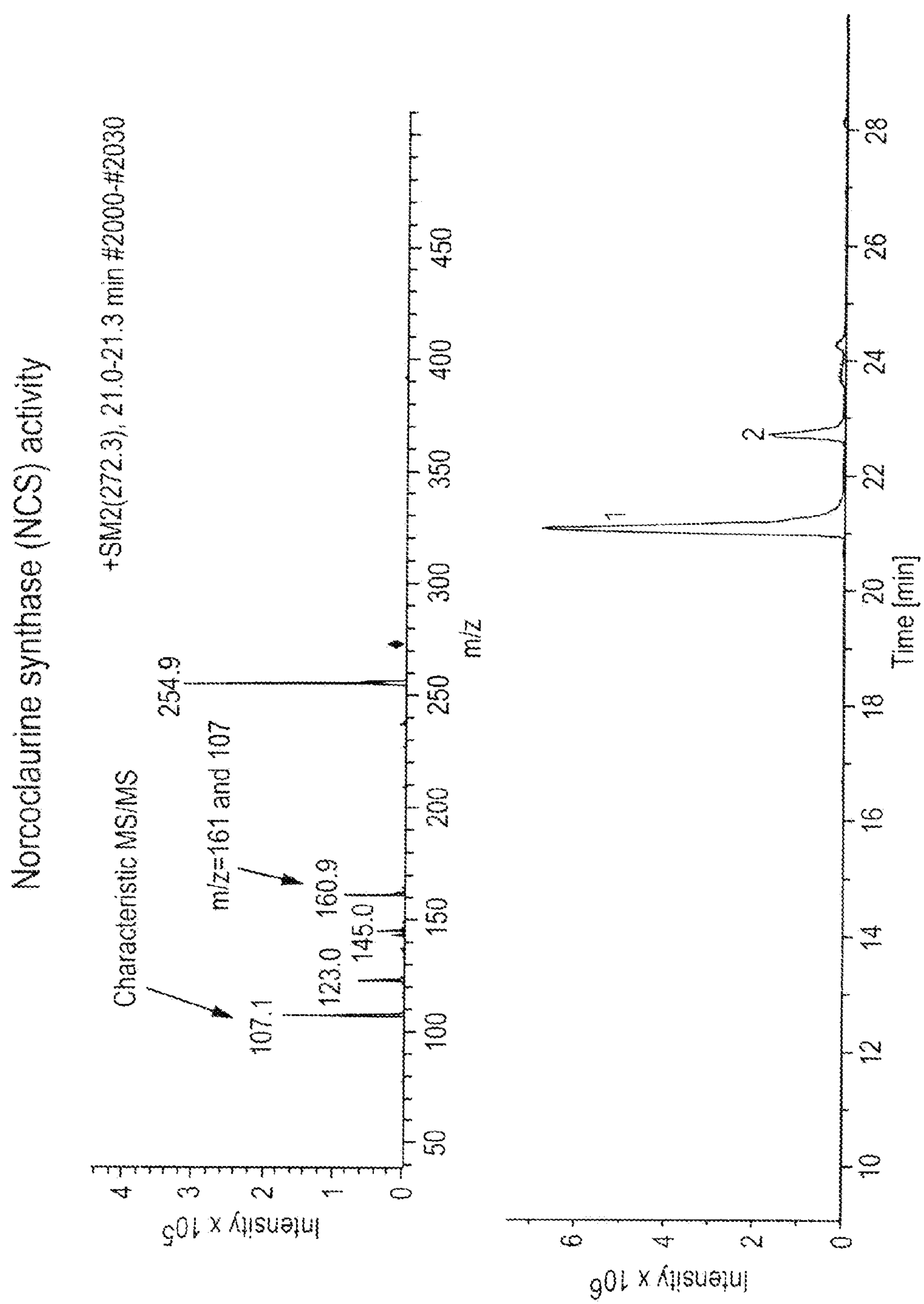

Norcoclaurine synthase (NCS) activity
+SM2(272.3), 21.0-21.3 min #2000-#2030
Characteristic MS/MS
m/z=161 and 107
107.1
123.0
145.0
160.9
254.9
Intensity x 10^5
m/z
Intensity x 10^6
Time [min]
1
2

FIG. 4B

# Production of (S)-reticuline from norlaudanosoline

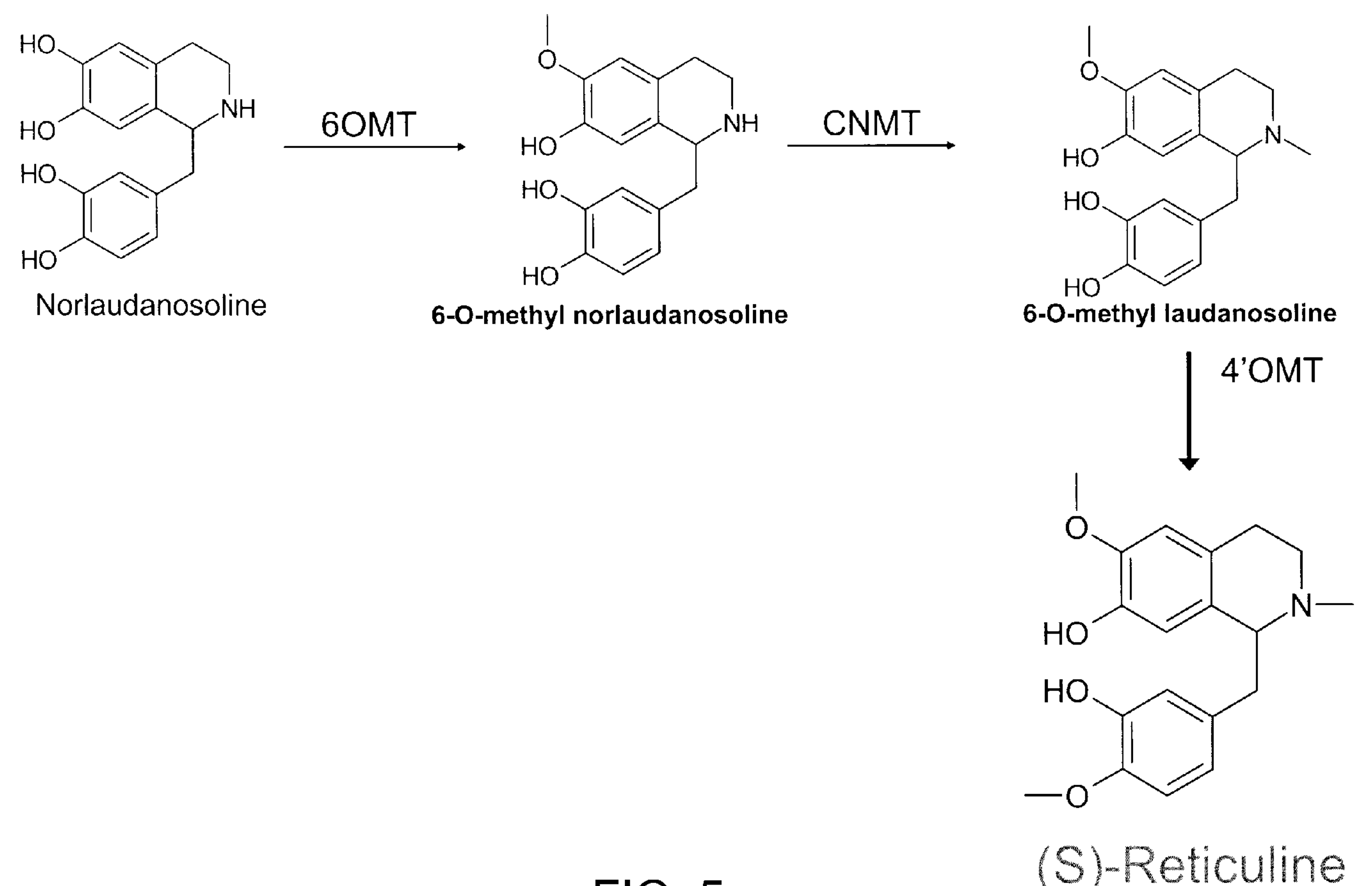



FIG. 5

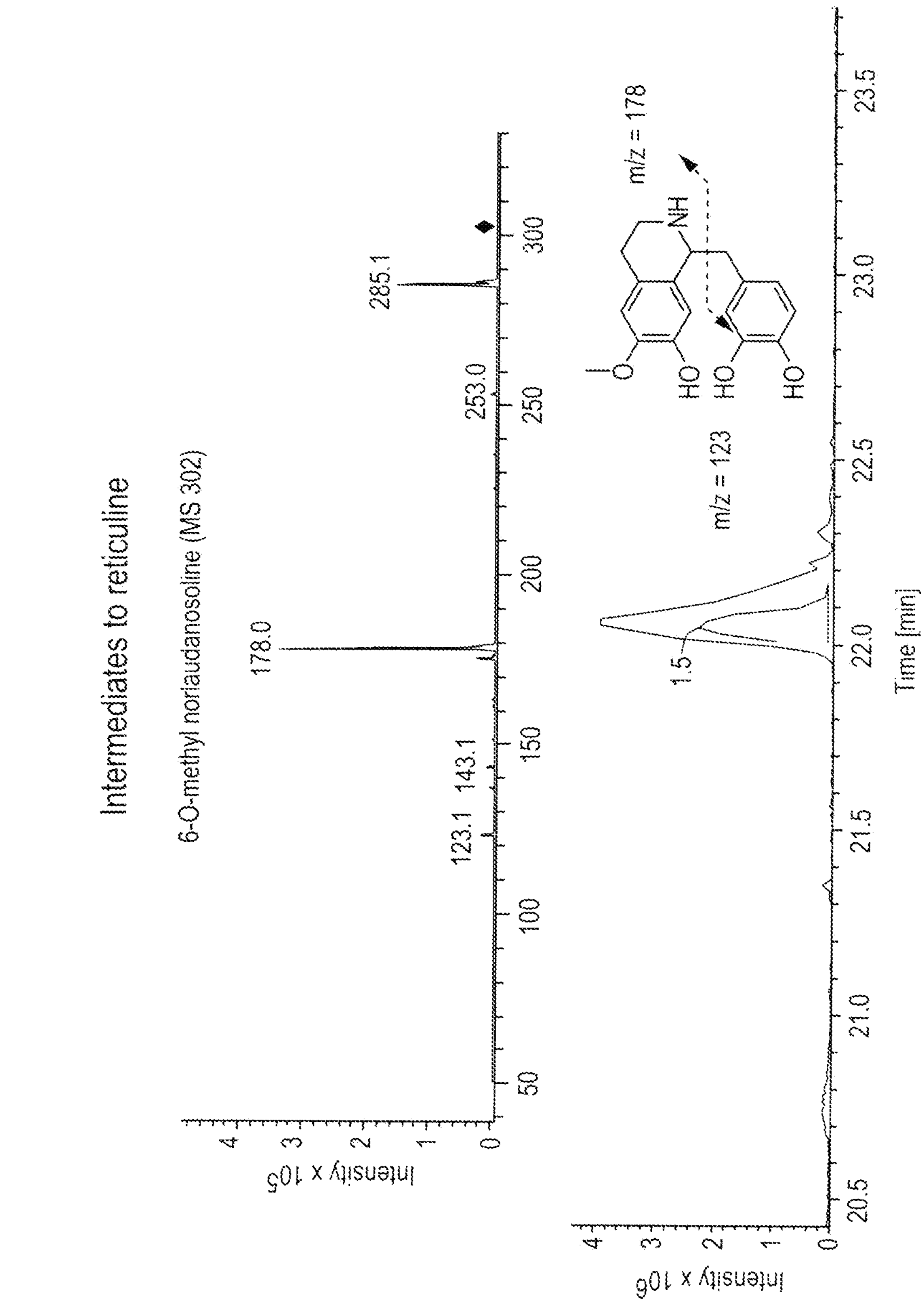

Intermediates to reticuline
6-O-methyl noriaudanosoline (MS 302)
123.1
143.1
178.0
253.0
285.1
Intensity x 10^5
m/z = 178
m/z = 123
NH
HO
HO
HO
1.5
Time [min]
Intensity x 10^6

FIG. 6A

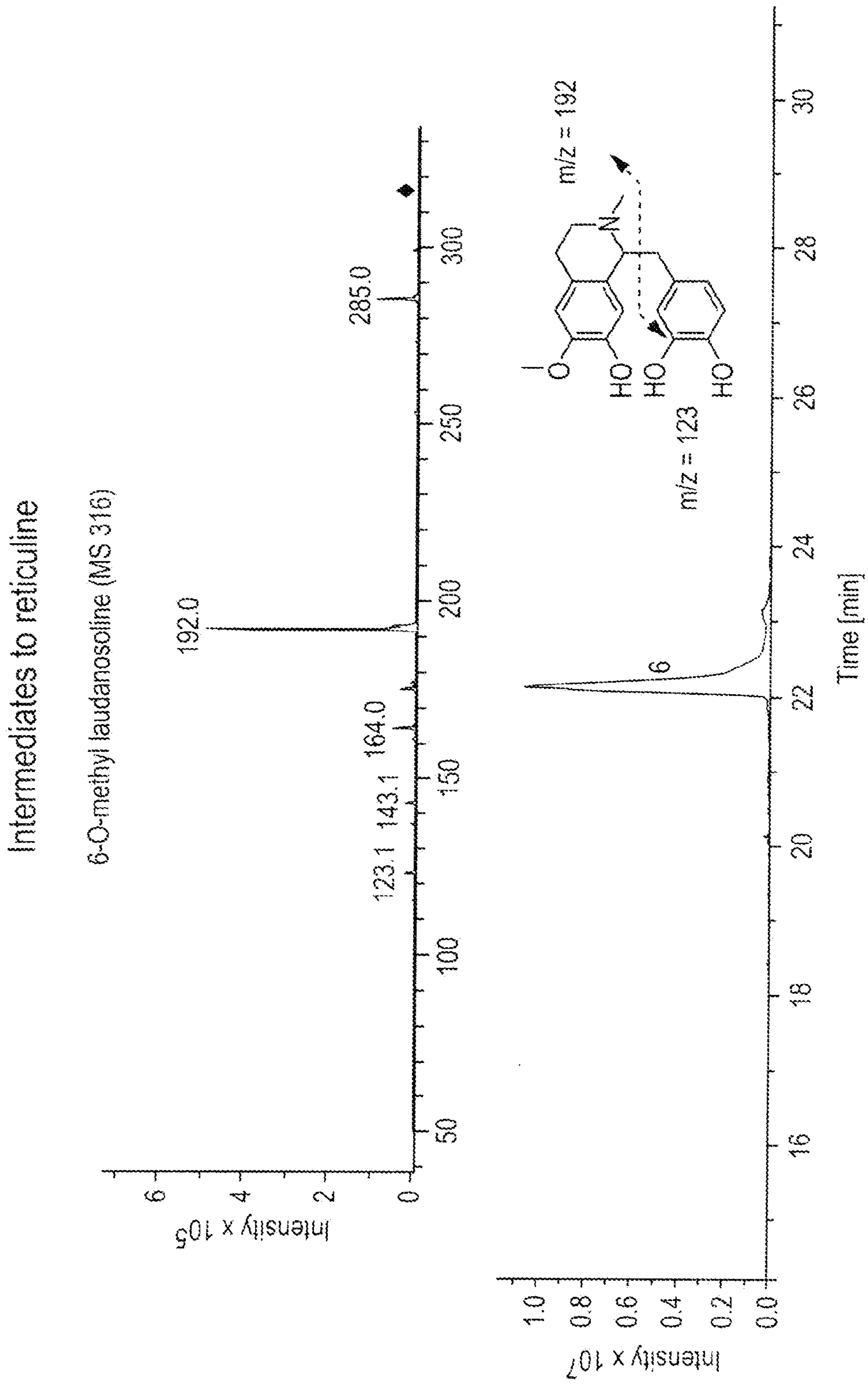

Intermediates to reticuline
6-O-methyl laudanosoline (MS 316)
192.0
285.0
123.1
143.1
164.0
Intensity x 10^5
m/z = 192
m/z = 123
HO
HO
HO
O
N
6
Time [min]
Intensity x 10^7

FIG. 6B

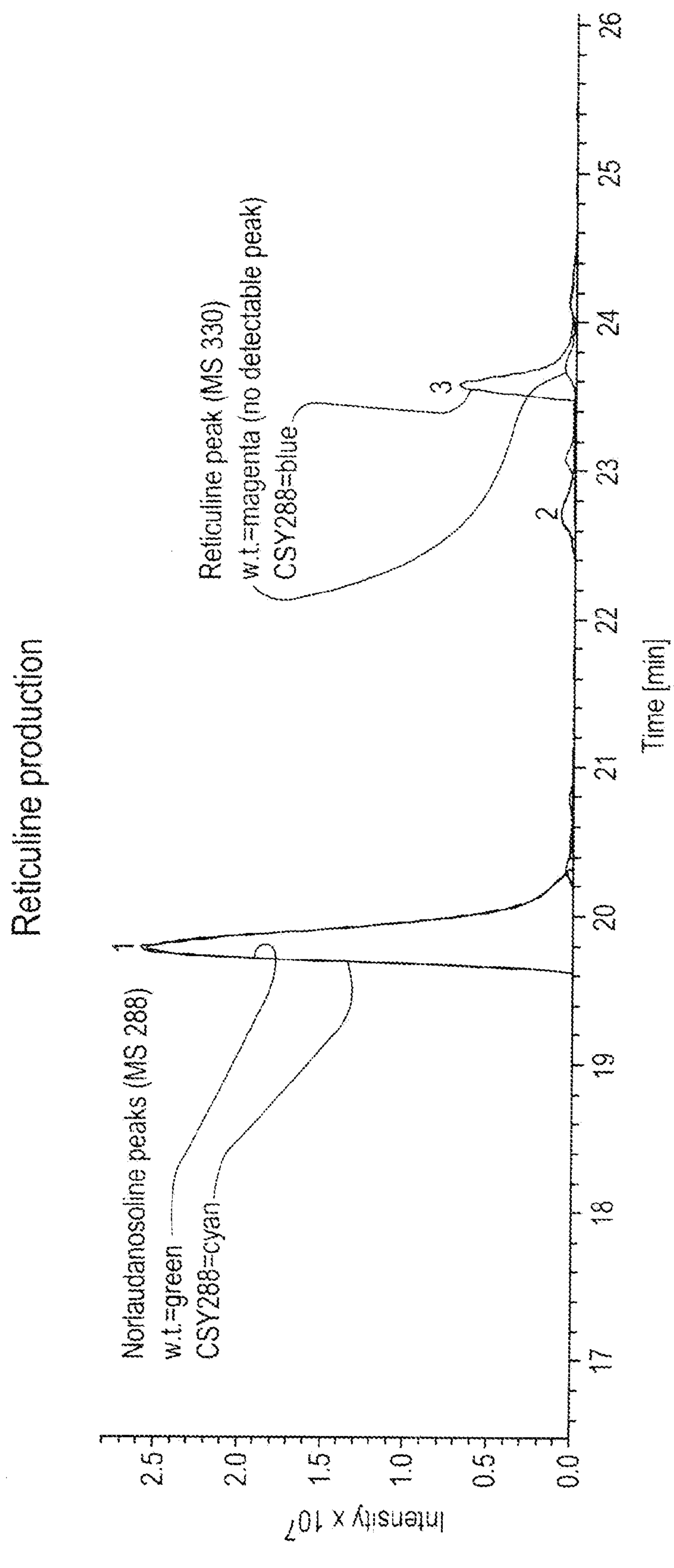

Reticuline production
Norlaudanosoline peaks (MS 288)
w.t.=green
CSY288=cyan
Reticuline peak (MS 330)
w.t.=magenta (no detectable peak)
CSY288=blue
1
2
3
Intensity x 10^7
0.0
0.5
1.0
1.5
2.0
2.5
Time [min]
17
18
19
20
21
22
23
24
25
26

FIG. 7

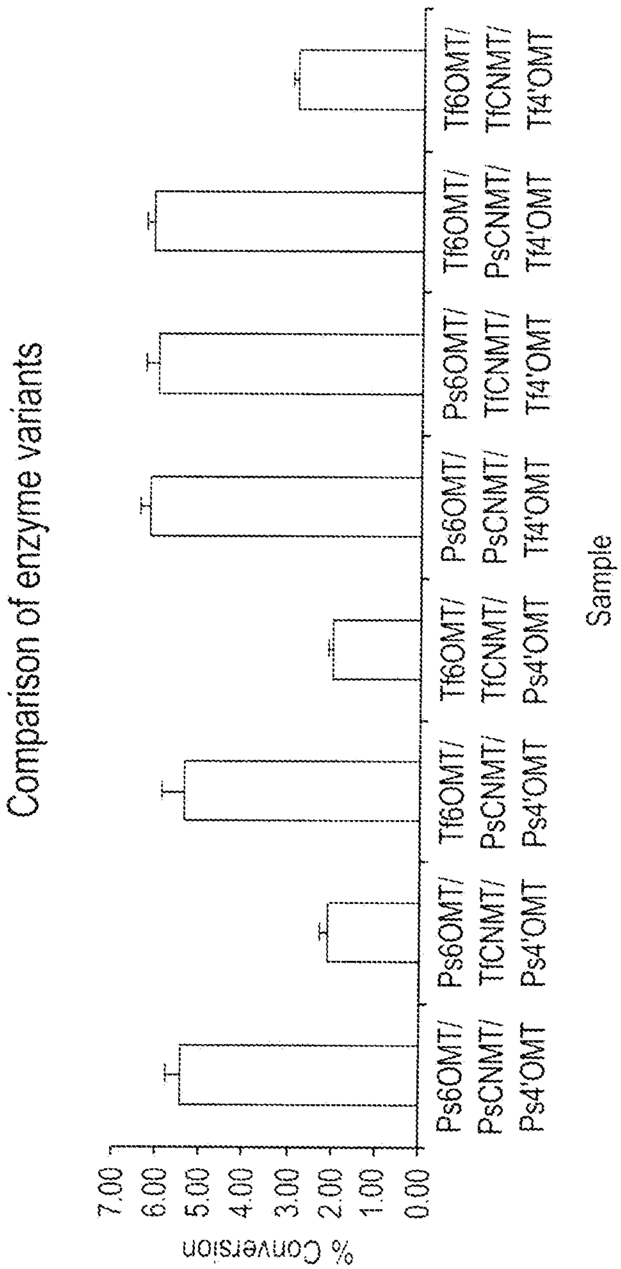

Comparison of enzyme variants
% Conversion
7.00
6.00
5.00
4.00
3.00
2.00
1.00
0.00
Ps6OMT/ PsCNMT/ Ps4'OMT
Ps6OMT/ TfCNMT/ Ps4'OMT
Tf6OMT/ PsCNMT/ Ps4'OMT
Tf6OMT/ TfCNMT/ Ps4'OMT
Ps6OMT/ PsCNMT/ Tf4'OMT
Ps6OMT/ TfCNMT/ Tf4'OMT
Tf6OMT/ PsCNMT/ Tf4'OMT
Tf6OMT/ TfCNMT/ Tf4'OMT
Sample

FIG. 8

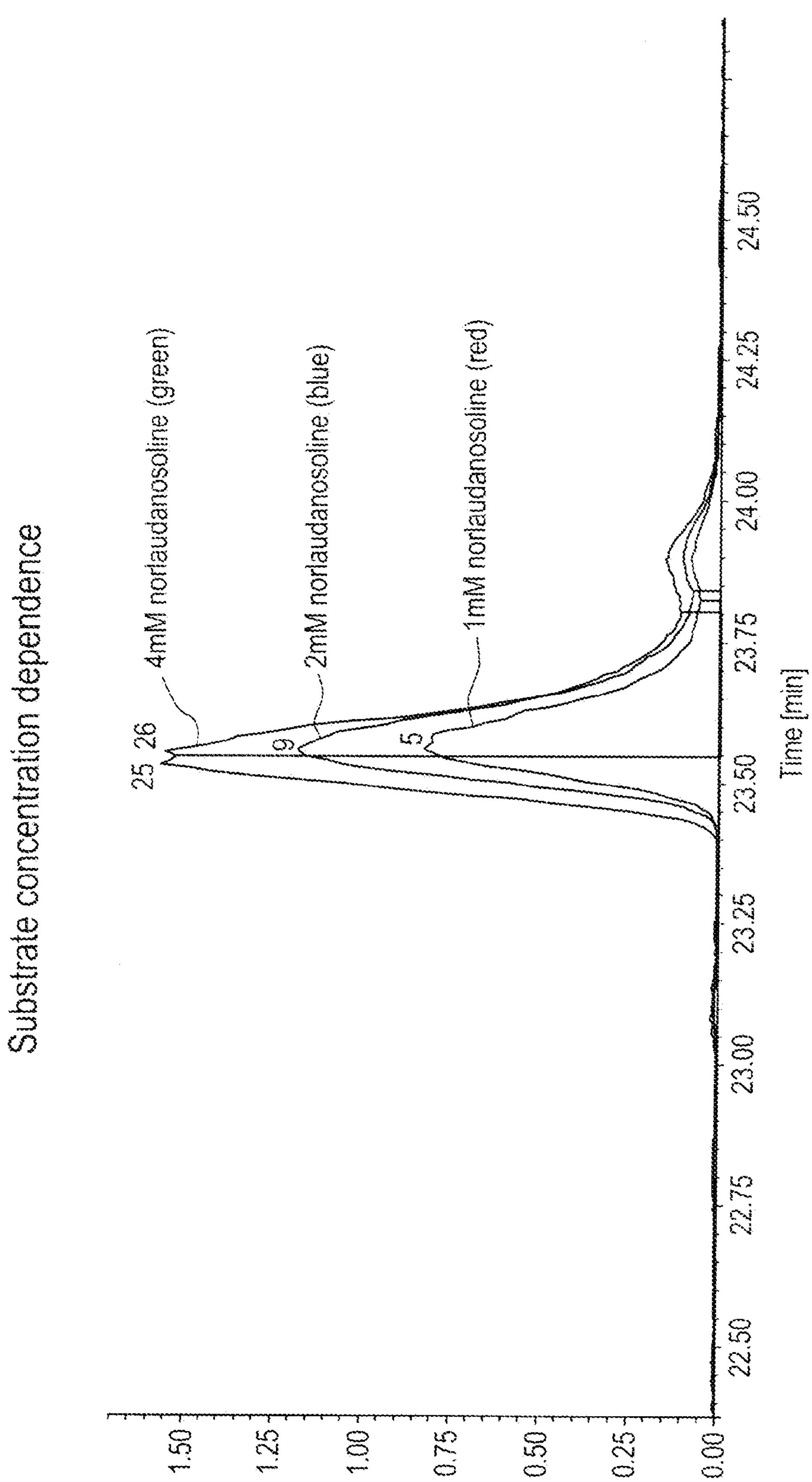

Substrate concentration dependence
4mM norlaudanosoline (green)
2mM norlaudanosoline (blue)
1mM norlaudanosoline (red)
25 26
9
5
Intensity x 10^8
0.00
0.25
0.50
0.75
1.00
1.25
1.50
Time [min]
22.50
22.75
23.00
23.25
23.50
23.75
24.00
24.25
24.50

FIG. 9

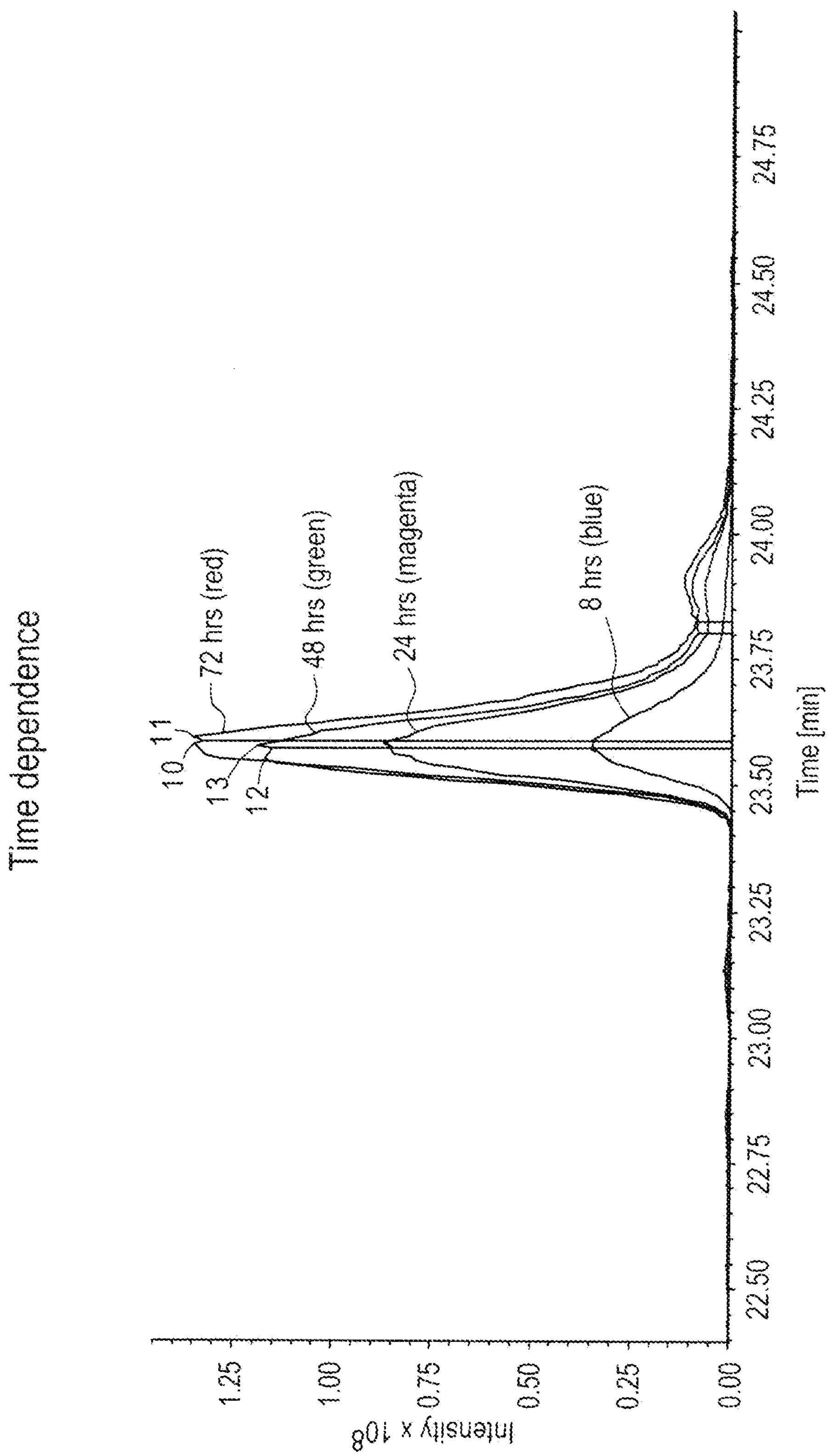

Time dependence
72 hrs (red)
48 hrs (green)
24 hrs (magenta)
8 hrs (blue)
10
11
12
13
Intensity x 10^8
0.00
0.25
0.50
0.75
1.00
1.25
Time [min]
22.50
22.75
23.00
23.25
23.50
23.75
24.00
24.25
24.50
24.75

FIG. 10

Plasmid-based expression v. chromosomal integration

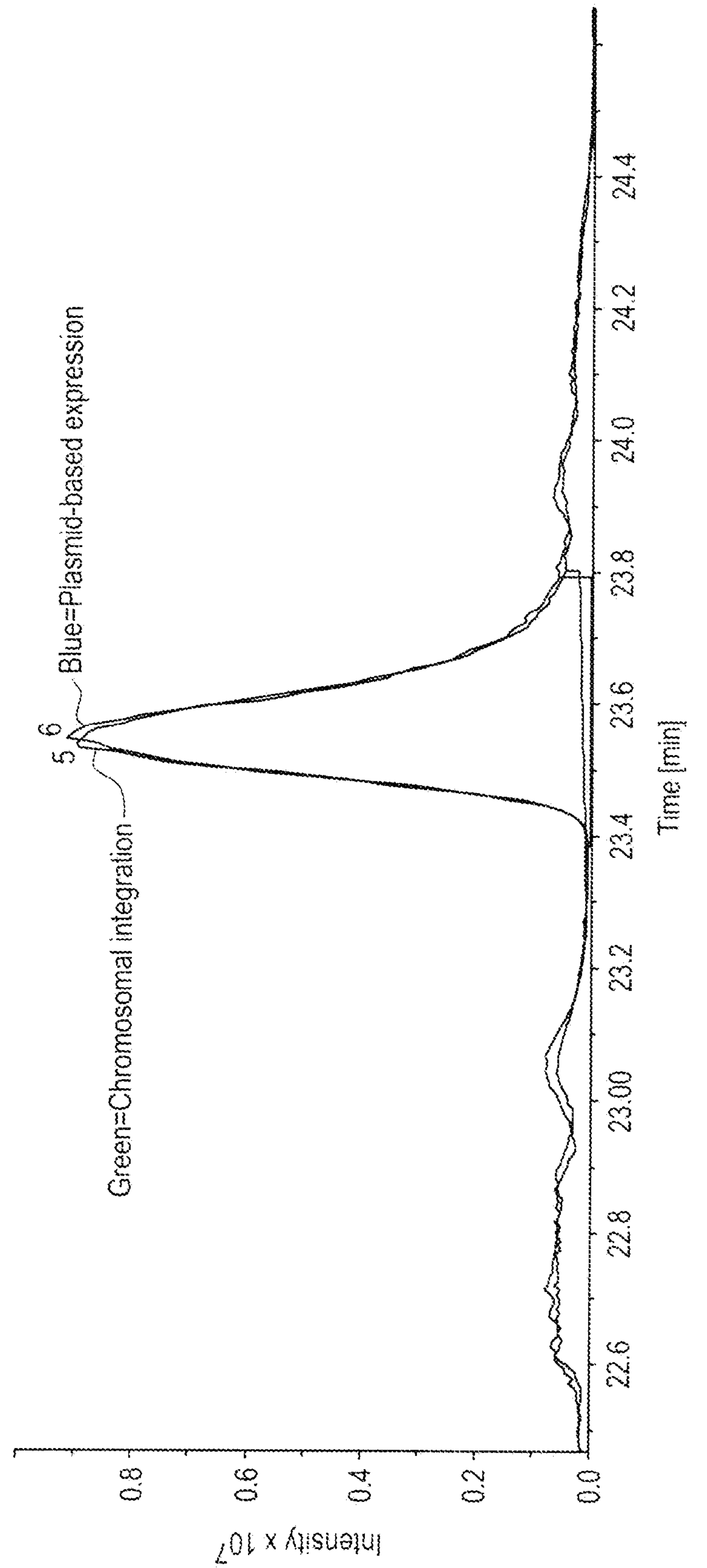



FIG. 11

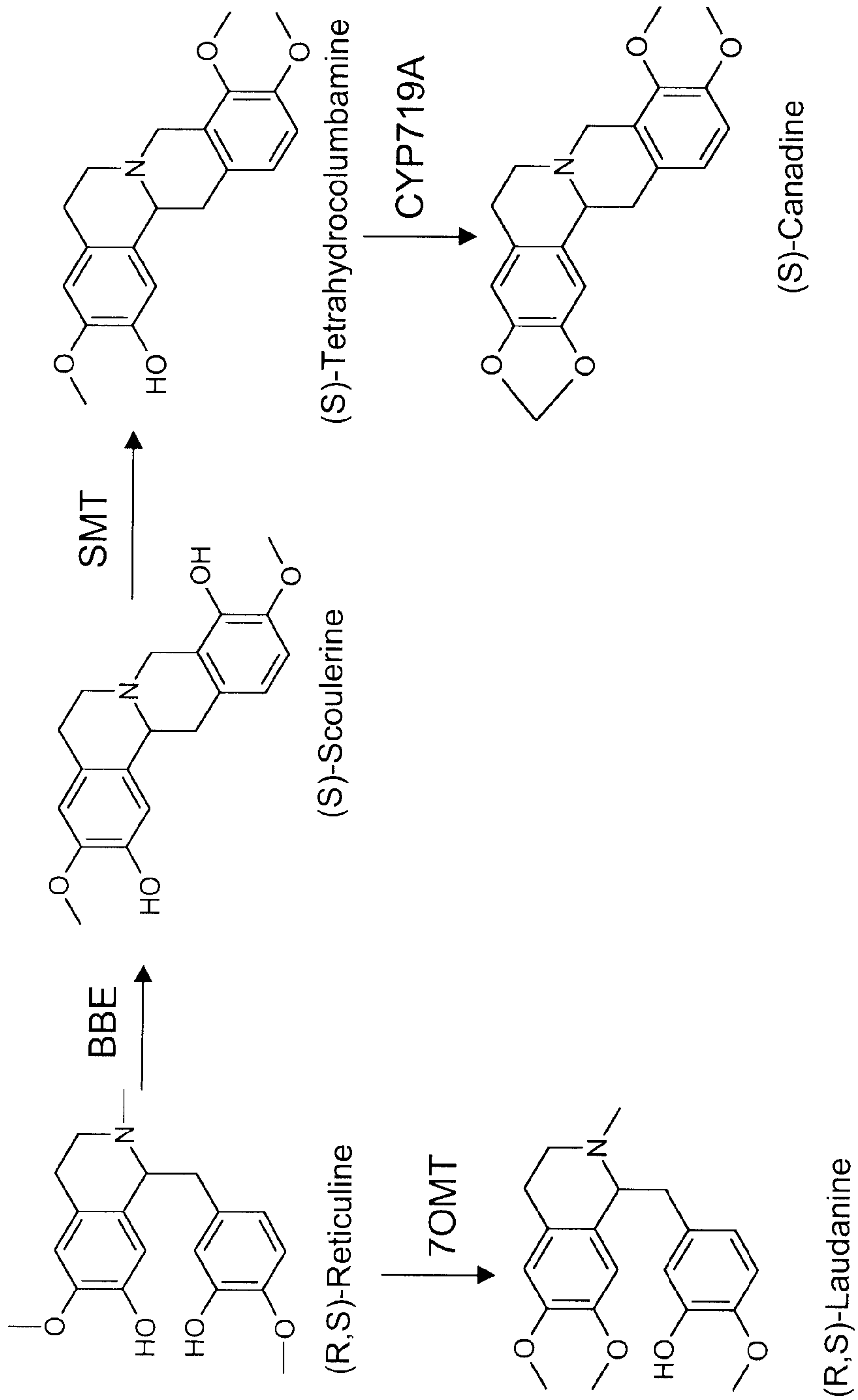

(R,S)-Reticuline
BBE
(S)-Scoulerine
SMT
(S)-Tetrahydrocolumbamine
CYP719A
(S)-Canadine
7OMT
(R,S)-Laudanine

FIG. 12

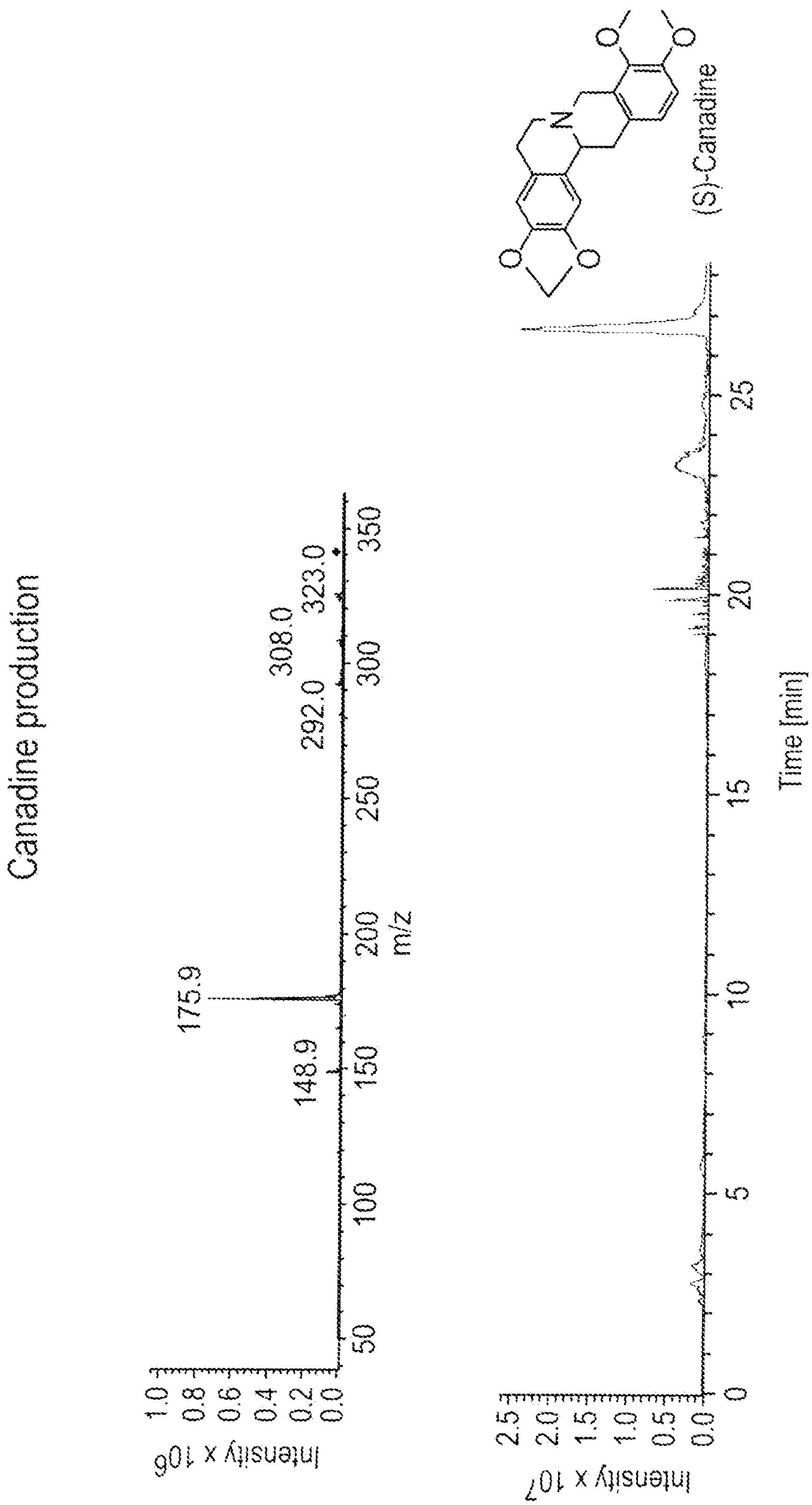

Canadine production
Intensity x 10^6
1.0
0.8
0.6
0.4
0.2
0.0
50
100
148.9
150
175.9
200
m/z
250
292.0
300
308.0
323.0
350
Intensity x 10^7
2.5
2.0
1.5
1.0
0.5
0.0
0
5
10
15
20
25
Time [min]
(S)-Canadine
N
O

FIG. 13A

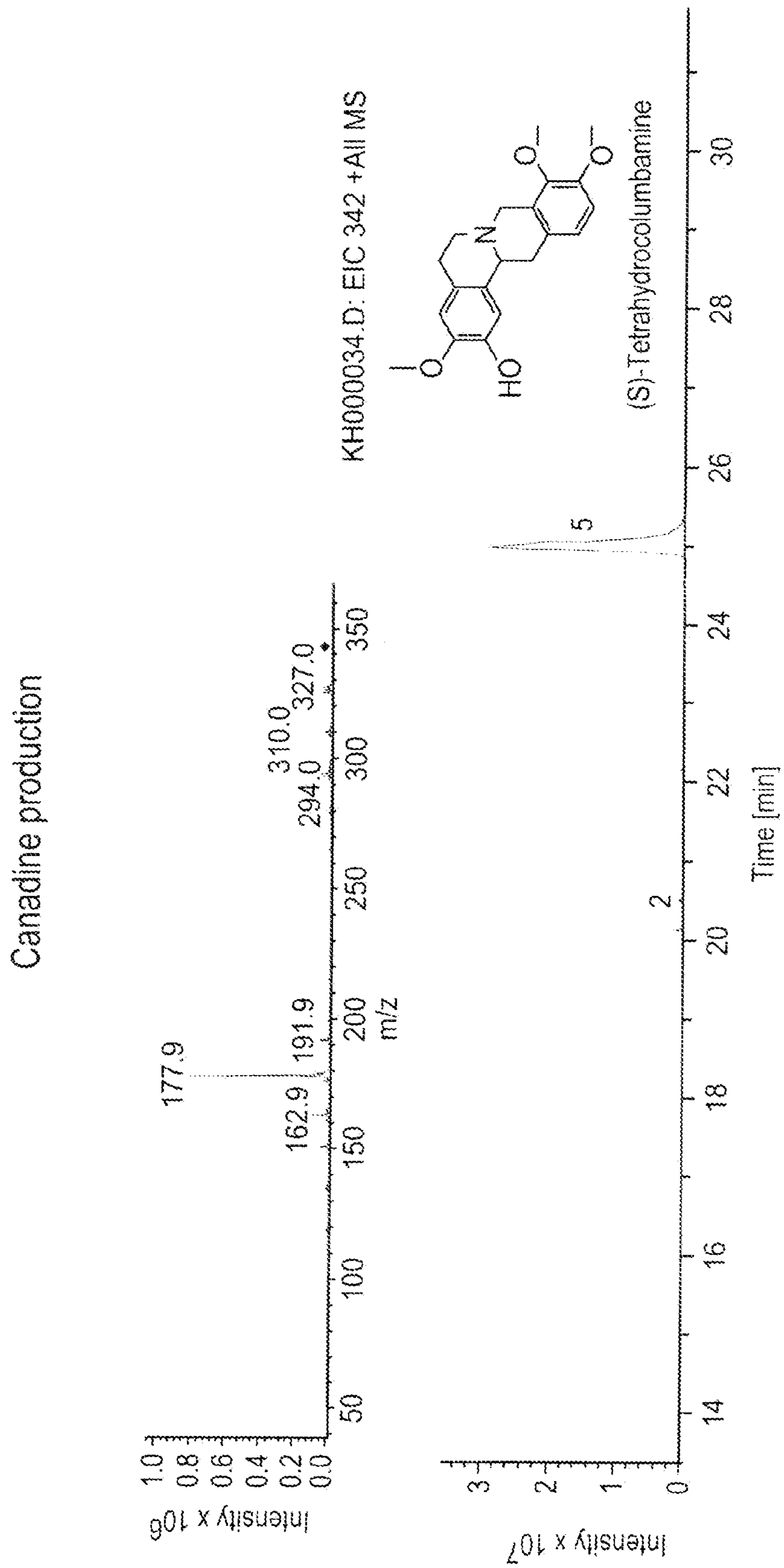
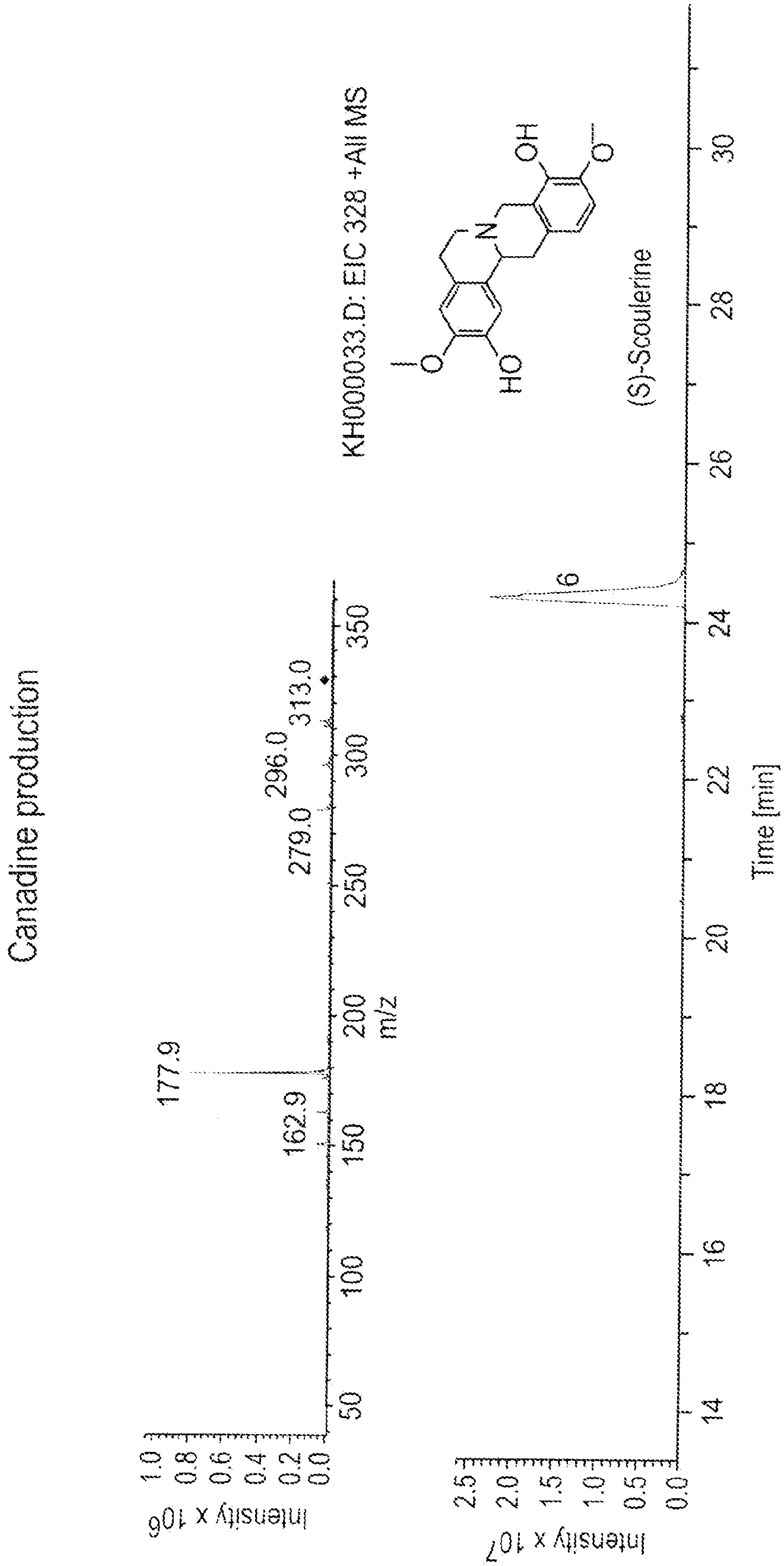

Canadine production
177.9
162.9
191.9
294.0
310.0
327.0
Intensity x 10^6
1.0
0.8
0.6
0.4
0.2
0.0
50
100
150
200
250
300
350
m/z
KH000034.D: EIC 342 +All MS
HO
N
(S)-Tetrahydrocolumbamine
5
2
Intensity x 10^7
3
2
1
0
14
16
18
20
22
24
26
28
30
Time [min]

FIG. 13B



Canadine production
177.9
162.9
279.0
296.0
313.0
m/z
50
100
150
200
250
300
350
Intensity x 10^6
1.0 0.8 0.6 0.4 0.2 0.0
KH000033.D: EIC 328 +All MS
HO
OH
N
(S)-Scoulerine
6
Time [min]
14 16 18 20 22 24 26 28 30
Intensity x 10^7
2.5 2.0 1.5 1.0 0.5 0.0


FIG. 13C

Canadine production

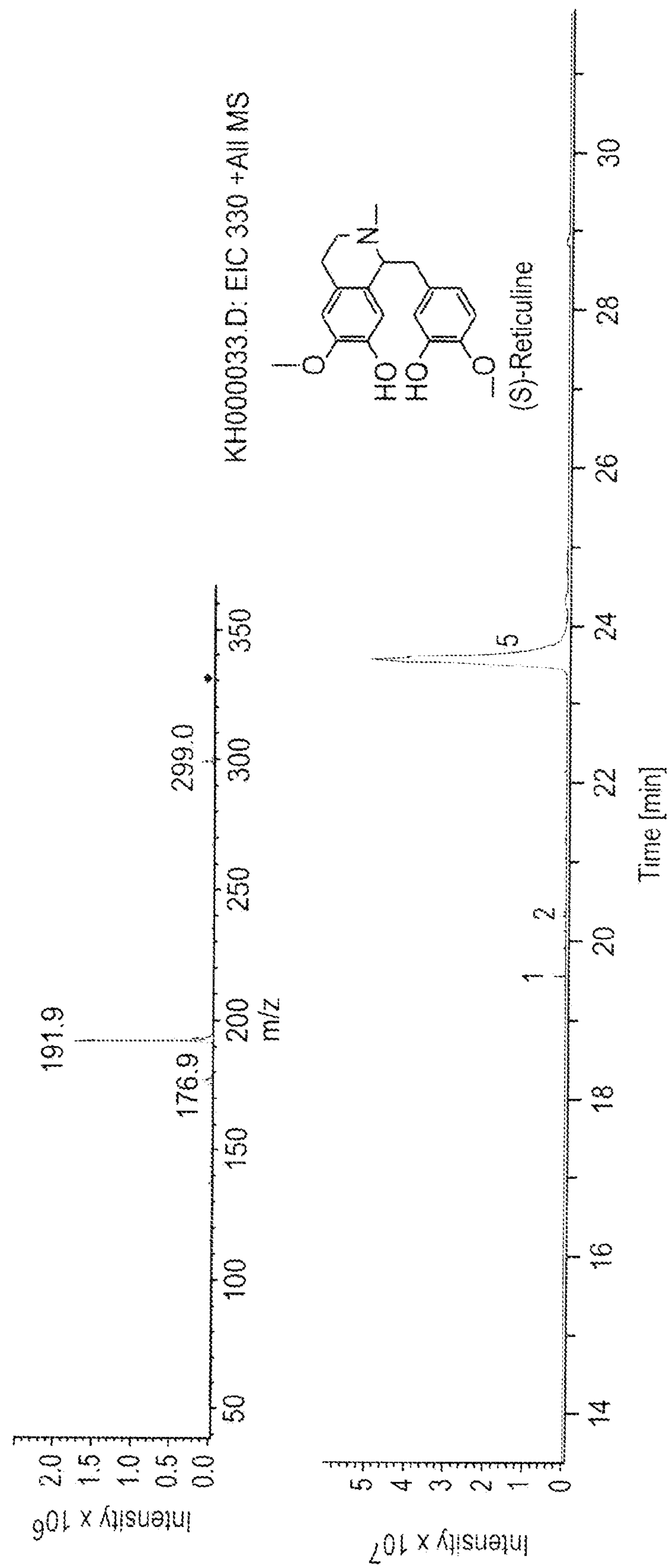



FIG. 13D

Morphinian alkaloids

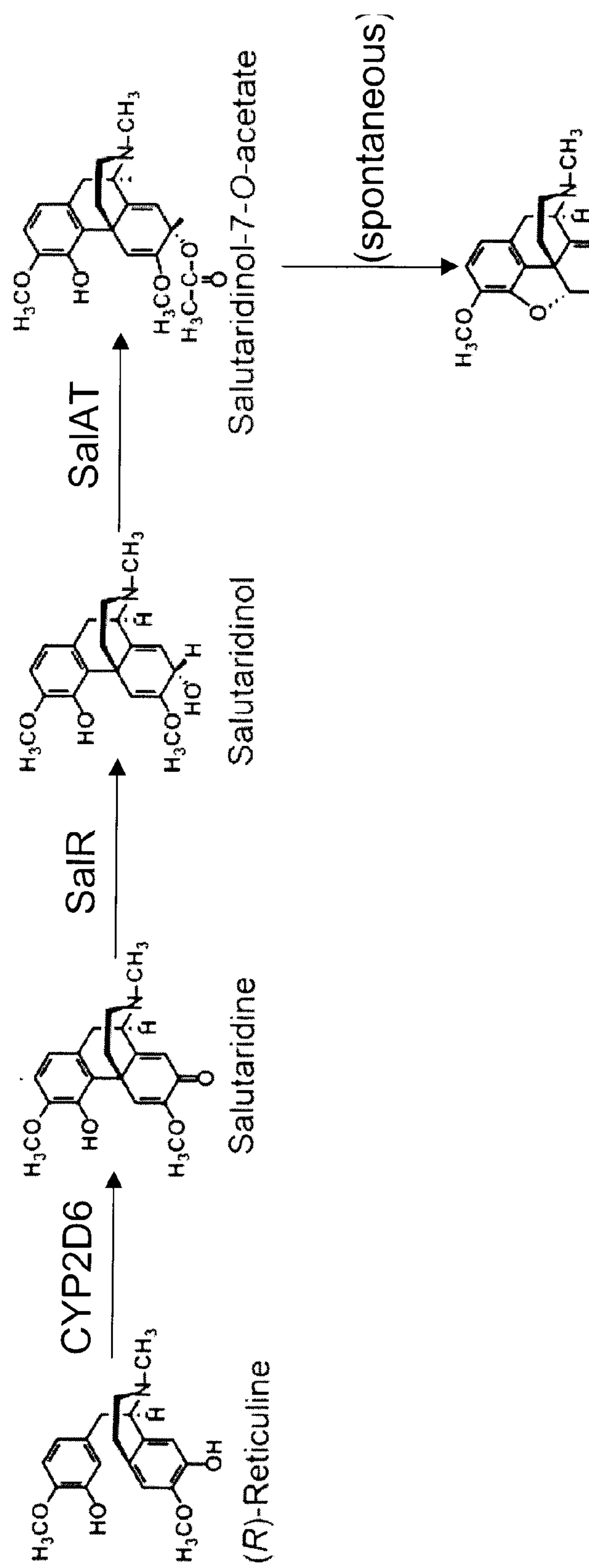



FIG. 14

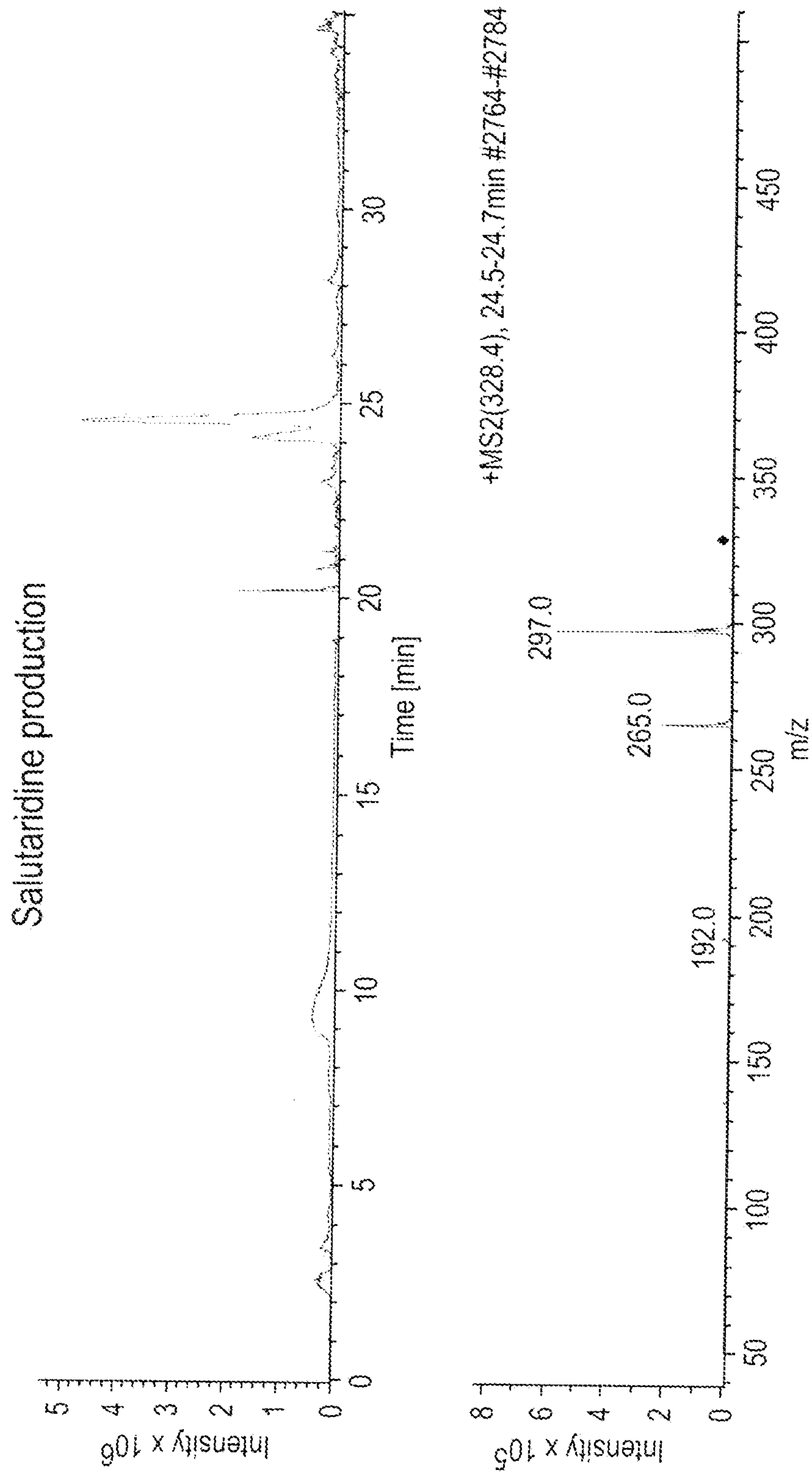

Salutaridine production
Intensity x 10^6
5 4 3 2 1 0
0 5 10 15 20 25 30
Time [min]
+MS2(328.4), 24.5-24.7min #2764-#2784
297.0
265.0
192.0
Intensity x 10^5
8 6 4 2 0
50 100 150 200 250 300 350 400 450
m/z

FIG. 15

# BIA Pathway Variations

| Sub-pathway | Substrate | Product | Example strain |
|---|---|---|---|
| A | tyrosine | dopamine | CSY235 |
| B | tyrosine | dopamine | CSY88 |
| C | tyrosine | 4-HPA | CSY104 |
| D | tyrosine | 4-HPA | CSY73 |
| E | dopamine + 4-HPA | norcoclaurine | CSY177 |
| F | norcoclaurine | reticuline | |
| G | norlaudanosoline | reticuline | CSY288 |
| H | laudanosoline | reticuline | CSY288 |
| I | reticuline | laudanine | CSY401 |
| J | reticuline | canadine | CSY410 |
| K | reticuline | thebaine | |
| L | laudanosoline | BIA #1 | |
| M | norlaudanosoline | laudanosoline | |
| N | norcoclaurine | laudanosoline | |
| O | norlaudanosoline | BIA #2 | |
| P | reticuline | BIA #3 | |
| Q | norcoclaurine | norlaudanosoline | |

FIG. 16A

# Combinations of BIA sub-pathways

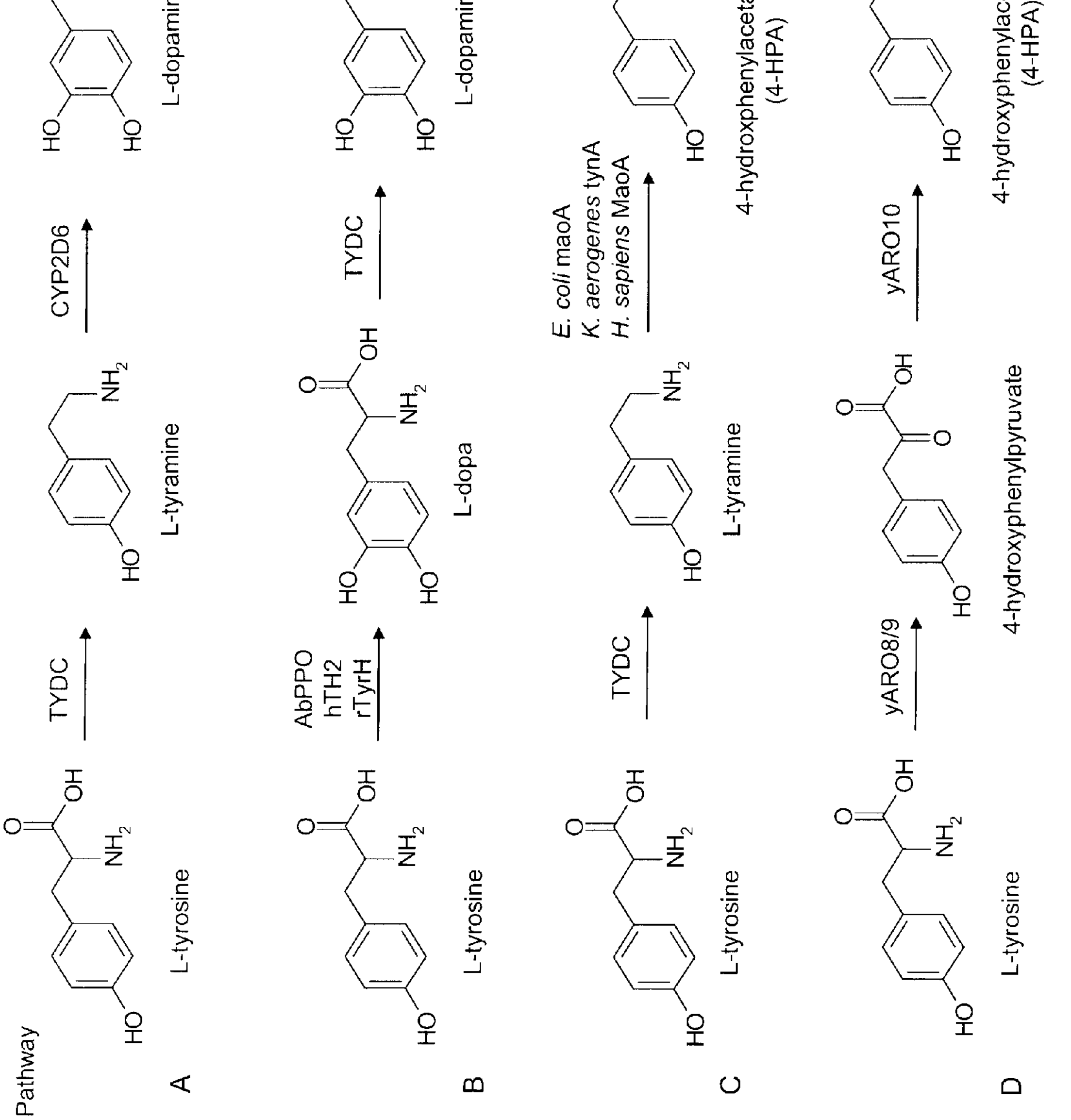
| Combinatorial pathway | Substrate | Product | Example strain |
|---|---|---|---|
| A + C + E + F + I | tyrosine | laudanine | |
| A + C + E + F + J | tyrosine | canadine | |
| A + C + E + F + K | tyrosine | thebaine | |
| B + C + E + F + I | tyrosine | laudanine | |
| B + C + E + F + J | tyrosine | canadine | |
| B + C + E + F + K | tyrosine | thebaine | |
| A + D + E + F + I | tyrosine | laudanine | |
| A + D + E + F + J | tyrosine | canadine | |
| A + D + E + F + K | tyrosine | thebaine | |
| B + D + E + F + I | tyrosine | laudanine | |
| B + D + E + F + J | tyrosine | canadine | |
| B + D + E + F + K | tyrosine | thebaine | |
| G + I | norlaudanosoline | laudanine | CSY401 |
| G + J | norlaudanosoline | canadine | CSY410 |
| G + K | norlaudanosoline | thebaine | |
| H + I | laudanosoline | laudanine | |
| H + J | laudanosoline | canadine | CSY410 |
| H + K | laudanosoline | thebaine | |

FIG. 16B

# Example combinations of BIA sub-pathways to produce non-natural alkaloids

| Combinatorial pathway | Substrate |
|---|---|
| M + L | norlaudanosoline |
| A + C + E + N + L | tyrosine |
| A + D + E + N + L | tyrosine |
| B + C + E + N + L | tyrosine |
| B + D + E + N + L | tyrosine |
| A + C + E + Q + O | tyrosine |
| A + D + E + Q + O | tyrosine |
| B + C + E + Q + O | tyrosine |
| B + D + E + Q + O | tyrosine |
| A + C + E + F + P | tyrosine |
| A + D + E + F + P | tyrosine |
| B + C + E + F + P | tyrosine |
| B + D + E + F + P | tyrosine |
| G + P | norlaudanosoline |
| H + P | laudanosoline |

FIG. 16C



Pathway
A
L-tyrosine
TYDC
L-tyramine
CYP2D6
L-dopamine
B
L-tyrosine
AbPPO
hTH2
rTyrH
L-dopa
TYDC
L-dopamine
C
L-tyrosine
TYDC
L-tyramine
E. coli maoA
K. aerogenes tynA
H. sapiens MaoA
4-hydroxphenylacetaldehyde (4-HPA)
D
L-tyrosine
yARO8/9
4-hydroxyphenylpyruvate
yARO10
4-hydroxyphenylacetaldehyde (4-HPA)


FIG. 16D

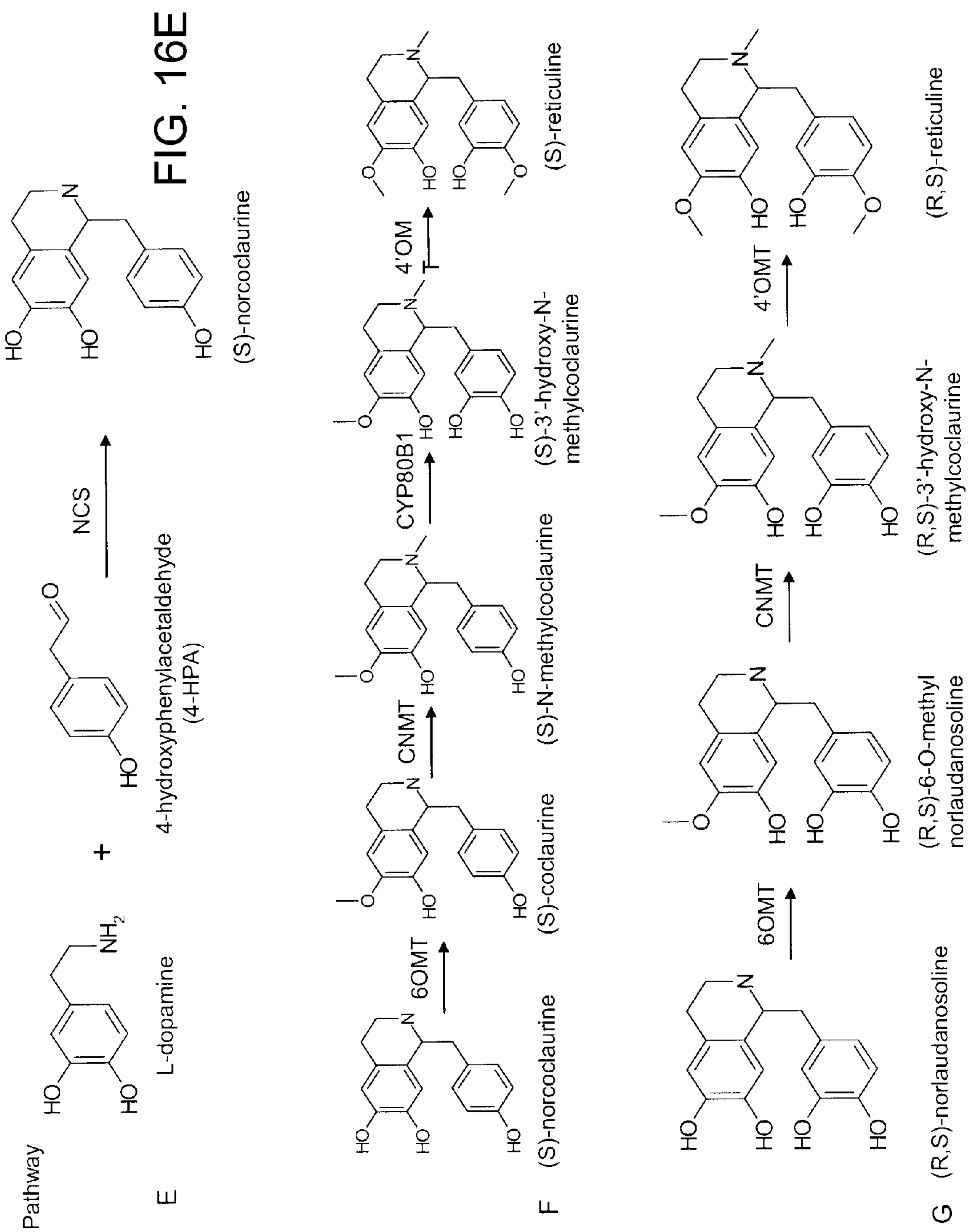

Pathway
E
L-dopamine
+
4-hydroxyphenylacetaldehyde
(4-HPA)
NCS
(S)-norcoclaurine
F
(S)-norcoclaurine
6OMT
(S)-coclaurine
CNMT
(S)-N-methylcoclaurine
CYP80B1
(S)-3'-hydroxy-N-methylcoclaurine
4'OMT
(S)-reticuline
G
(R,S)-norlaudanosoline
6OMT
(R,S)-6-O-methyl norlaudanosoline
CNMT
(R,S)-3'-hydroxy-N-methylcoclaurine
4'OMT
(R,S)-reticuline

FIG. 16E

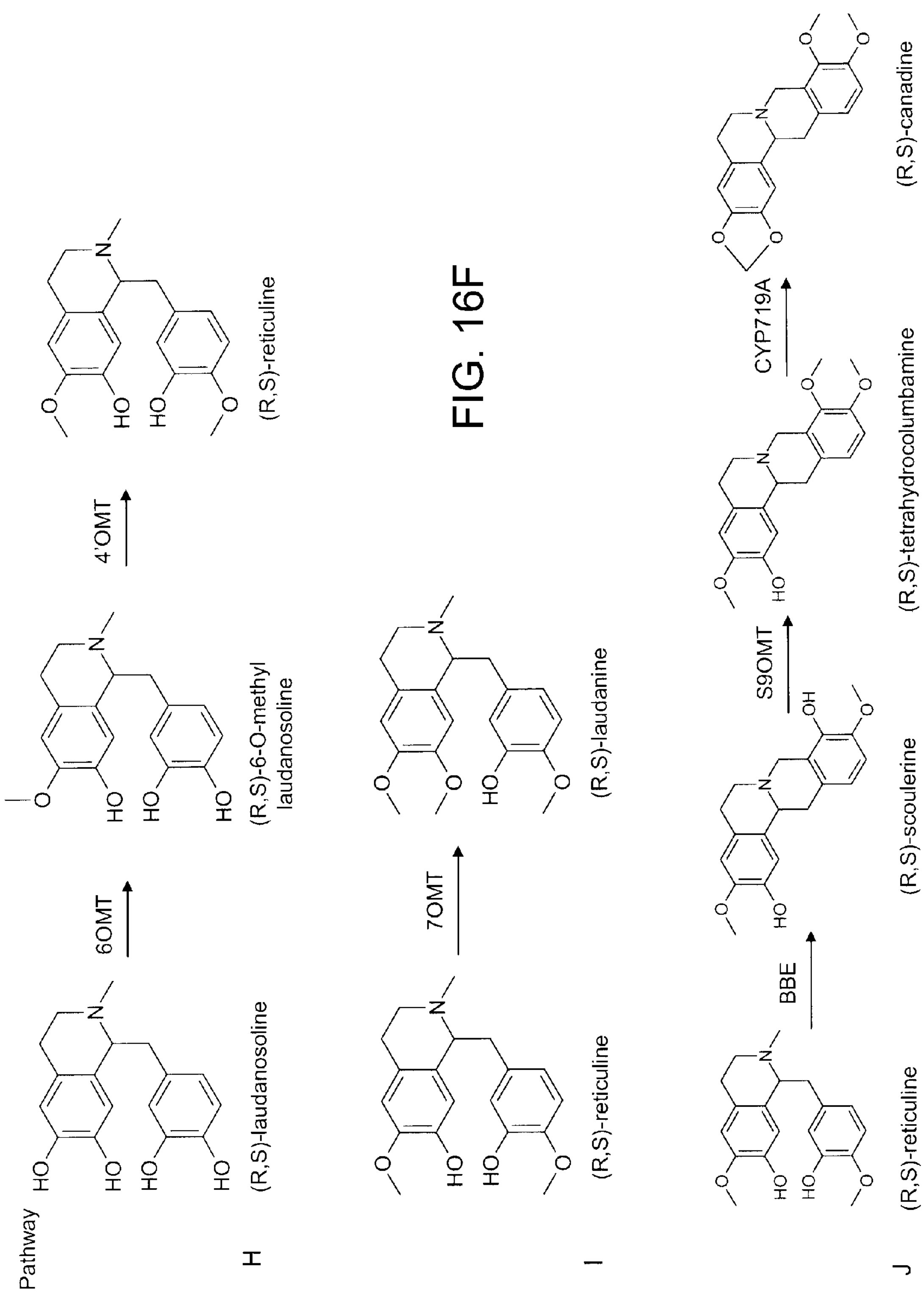

Pathway
H
(R,S)-laudanosoline
6OMT
(R,S)-6-O-methyl laudanosoline
4'OMT
(R,S)-reticuline
I
(R,S)-reticuline
7OMT
(R,S)-laudanine
J
(R,S)-reticuline
BBE
(R,S)-scoulerine
S9OMT
(R,S)-tetrahydrocolumbamine
CYP719A
(R,S)-canadine

FIG. 16F

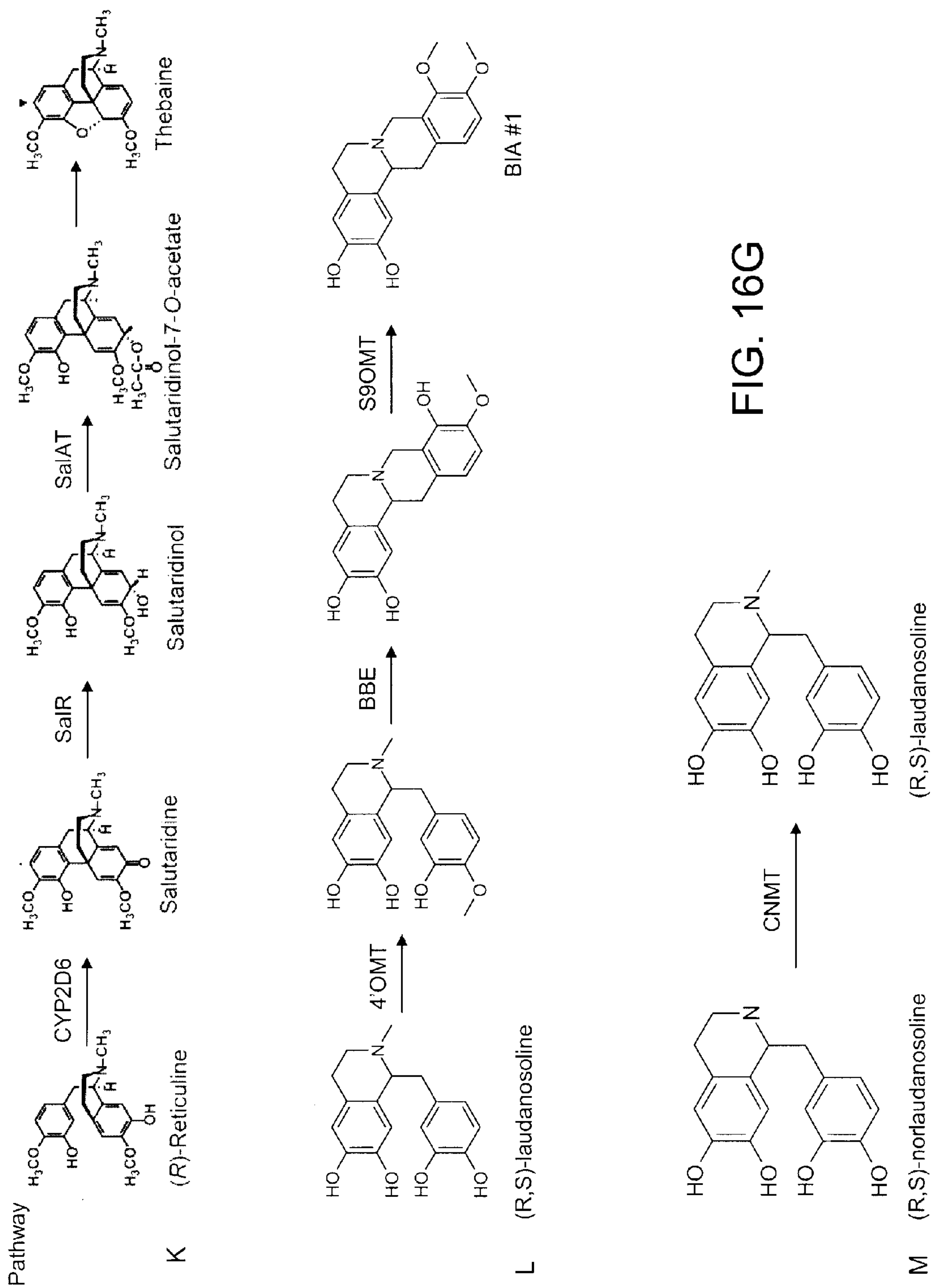

Pathway
K
(R)-Reticuline
CYP2D6
Salutaridine
SalR
Salutaridinol
SalAT
Salutaridinol-7-O-acetate
Thebaine
L
(R,S)-laudanosoline
4'OMT
BBE
S9OMT
BIA #1
M
(R,S)-norlaudanosoline
CNMT
(R,S)-laudanosoline

FIG. 16G

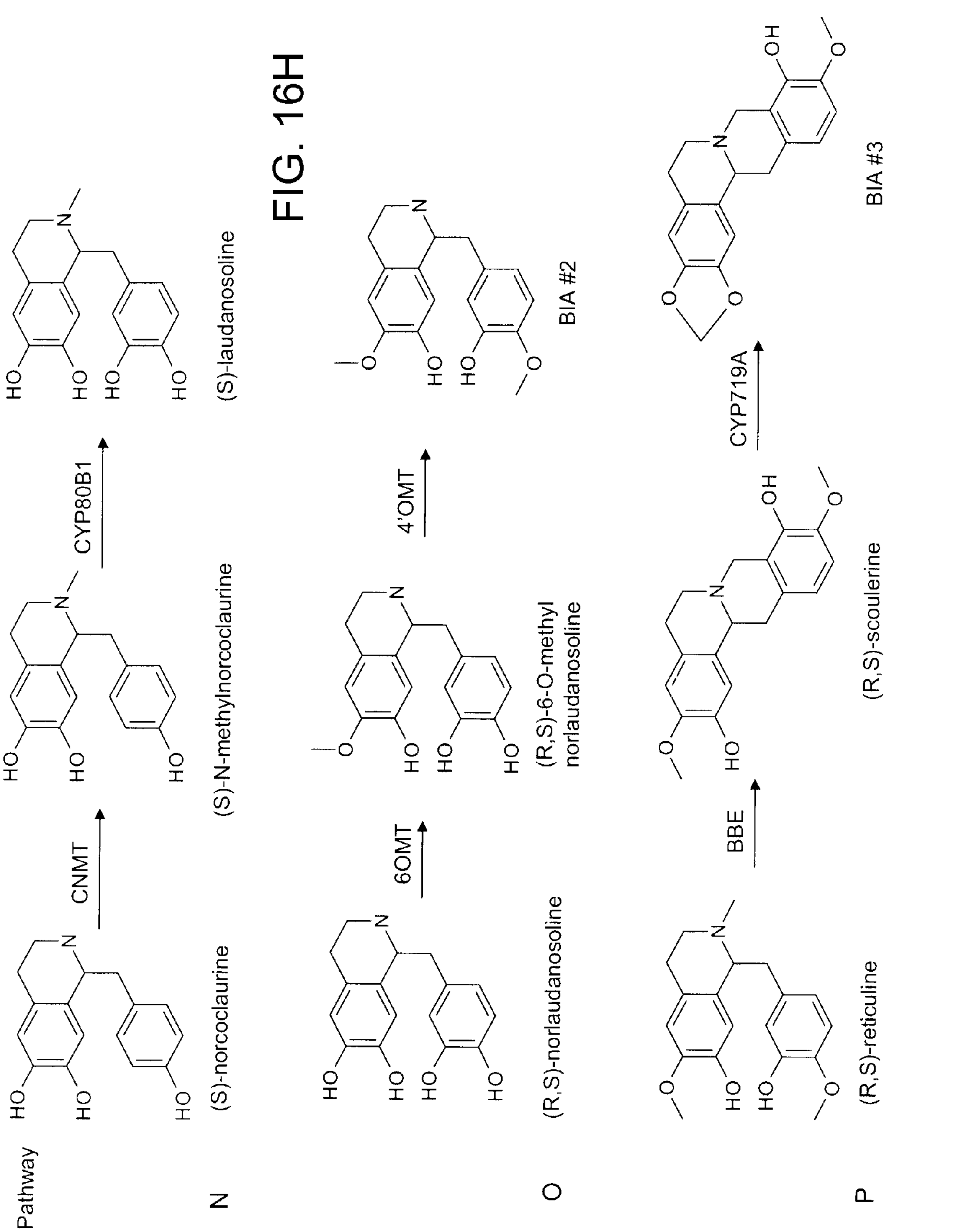

Pathway
N
(S)-norcoclaurine
CNMT
(S)-N-methylnorcoclaurine
CYP80B1
(S)-laudanosoline
O
(R,S)-norlaudanosoline
6OMT
(R,S)-6-O-methyl norlaudanosoline
4'OMT
BIA #2
P
(R,S)-reticuline
BBE
(R,S)-scoulerine
CYP719A
BIA #3

FIG. 16H

Pathway

Q

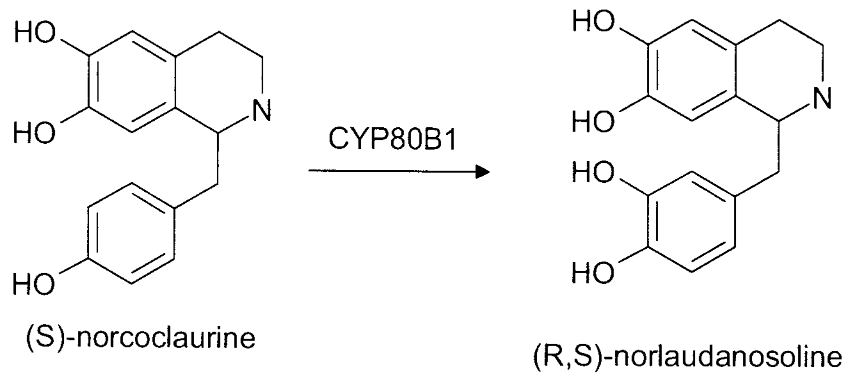



FIG. 16I

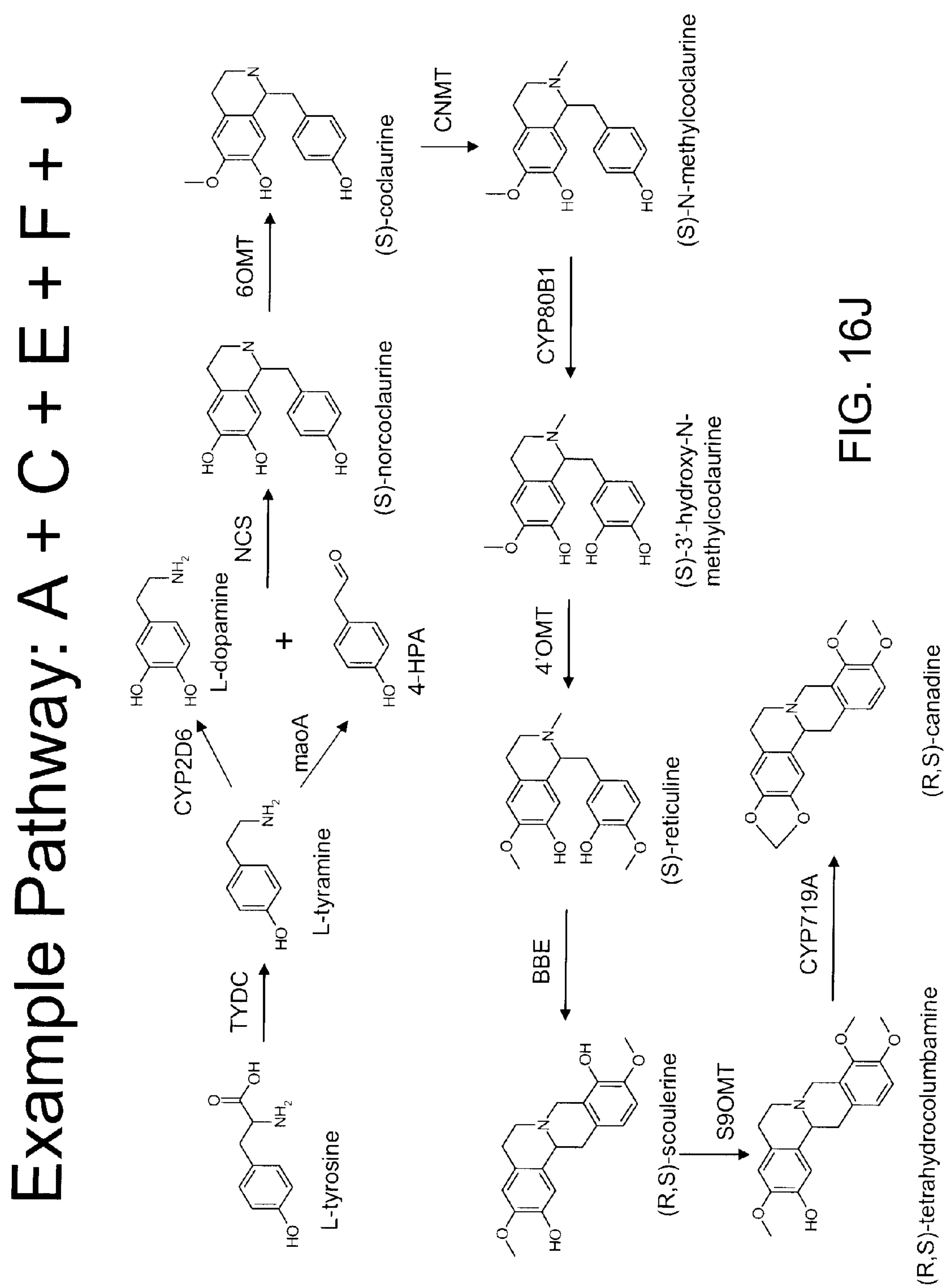

Example Pathway: A + C + E + F + J
L-tyrosine
TYDC
L-tyramine
CYP2D6
maoA
L-dopamine
4-HPA
NCS
(S)-norcoclaurine
6OMT
(S)-coclaurine
CNMT
(S)-N-methylcoclaurine
CYP80B1
(S)-3'-hydroxy-N-methylcoclaurine
4'OMT
(S)-reticuline
BBE
(R,S)-scoulerine
S9OMT
(R,S)-tetrahydrocolumbamine
CYP719A
(R,S)-canadine

FIG. 16J

# COMPOSITIONS AND METHODS FOR PRODUCING BENZYLISOQUINOLINE ALKALOIDS

## CROSS-REFERENCE TO RELATED APPLICATIONS

The application is a divisional application of U.S. patent application Ser. No. 11/875,814, filed Oct. 19, 2007; which claims priority to U.S. Provisional Application No. 60/859,149, filed Nov. 15, 2006; and 60/852,954 filed Oct. 19, 2006, each of which are incorporated by reference in their entirety.

## STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

This invention was made with government support under Grant No. GM077346 awarded by the National Institutes of Health. The government has certain rights in the invention.

## BACKGROUND OF THE INVENTION

1. Field of the Invention

The invention relates to compositions and methods for producing benzylisoquinoline alkaloids (BIAs) or molecules involved in the production of BIAs. The compositions comprise host cells comprising at least one heterologous coding sequence that encodes for an enzyme or its equivalent that is involved in the BIA synthetic pathway.

2. Background of the Invention

Alkaloids are a diverse group of nitrogen-containing small molecules that are produced in plants, marine organisms, and microorganisms through complex biosynthetic pathways. These complex molecules exhibit a range of interesting pharmacological activities and have been used as antimalarials, anticancer agents, analgesics, and in treatment of parkinsonism, hypertension, and central nervous system disorders.

The benzylisoquinoline alkaloids (BIAs) are a family of alkaloid molecules with over 2,500 defined structures. The most common BIAs currently utilized as medicinal compounds are synthesized in the opium poppy and include the analgesics codeine and morphine. However, many intermediates in this pathway that do not accumulate to significant levels in plants are themselves pharmacologically active as analgesics, antimalarials, anticancer agents, and antimicrobial agents. Even for molecules that accumulate to high levels in plants, it would be advantageous to eliminate the rigorous extraction and purification procedures required to isolate these compounds.

Chemical synthesis of these types of molecules is normally a costly and time-consuming process, often requiring harsh process conditions, generating toxic waste streams, and resulting in low quantities of the chemicals. In addition, many structures are simply unattainable using traditional synthesis methods due to the number of chiral centers and reactive functional groups. Alternatively, the production of BIAs can be achieved at relatively low cost and high yields in a microbial host. This will allow for cost-effective large scale production of intermediate and end-product BIAs.

The inventors have developed methods and compounds for the production of complex BIAs and their intermediates. Specifically, one can generate these molecules by expressing cloned and synthetic cDNAs in the host organism such that precursor molecules naturally produced in yeast, specifically L-tyrosine, are converted to various BIA intermediates in these engineered strains through a series of specific reactions catalyzed by recombinant enzymes. Engineered yeast strains can also be used to convert more complex substrates into value-added BIA molecules using similar strategies. The novel technology developed is the production of this family of alkaloid molecules in yeast from simple precursor molecules and/or more complex substrates using yeast or another microorganism as a host for the production of these molecules. Various BIA intermediates will be produced in yeast and can be used directly for their pharmacological activities or they can be used as starting molecules for chemical synthesis modifications to place additional functional groups on these backbone molecules to alter their pharmacological activities. For instance, one important intermediate reticulin is a molecule from which a number of pharmacologically active molecules such as sanguinarine and codeine can be synthesized. In addition, host cells can be engineered to produce non-natural alkaloid derivatives by adding novel enzymatic conversion steps to the heterologous pathway or eliminating steps from the native or heterologous pathway.

Microbial biosynthesis enables green synthesis and the production of these molecules without extreme reaction conditions and toxic waste streams. Furthermore, many intermediates of interest do not accumulate in the native plant hosts, and studies have demonstrated that modifying expression of specific genes in this pathway in the native plant hosts in order to direct accumulation of specific intermediates often inactivates multiple enzymes in the pathway, prohibiting the rational engineering of plant strains to accumulate specific intermediates. Microbial biosynthesis also eliminates the need for rigorous extraction and purification procedures required to isolate target molecules from the native host.

## SUMMARY OF THE INVENTION

The present invention relates to host cells that produce compounds classified as benzylisoquinoline alkaloids, as well as select precursors and intermediates thereof. The host cells comprise one, two or more heterologous coding sequences wherein each of the heterologous coding sequences encodes an enzyme involved in the metabolic pathway of a benzylisoquinoline, or its precursors or intermediates from a starting compound. The invention also relates to methods of producing the benzylisoquinoline, as well as select precursors and intermediates thereof by culturing the host cells under conditions that promote expression and activity of the necessary enzymes that produce the benzylisoquinoline or precursors or intermediates thereof, as well as optimize the growth rate of the host.

## BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** depicts a synthetic pathway present in the host cells of the present invention. The pathway begins with tyrosine and ends with reticuline. The pathway can include fewer enzymes than those displayed if the desired end result is one of the intermediates in the tyrosine→reticuline pathway.

FIG. **2** depicts measurement of dopamine production from a culture of host cells of the present invention.

FIG. **3** depicts alternative pathways for 4-HPA production from tyrosine through either tyramine or 4-hydroxyphenylpyruvate.

FIGS. **4**A and **4**B depict measurement of norcoclaurine production from a culture of host cells of the present invention. In this particular culture, the cells possessed the NCS heterologous coding sequence and the growth media was supplemented with dopamine and 4-HPA. FIG. **4**A shows the pathway of norcoclaurine production and FIG. **4**B shows the chromatogram confirming production of norcoclaurine.

FIG. **5** depicts the synthetic pathway present in embodiments of host cells in the present invention. The pathway begins with norlaudanosoline and ends with reticuline. The pathway can include fewer enzymes than those displayed if the desired end result is one of the intermediates in the norlaudanosoline→reticuline pathway.

FIGS. **6**A and **6**B depict the measurement of intermediates in the norlaudanosoline→reticuline pathway. FIG. **6**A shows the levels of methyl norlaudanosoline produced, and FIG. **6**B shows the levels of methyllaudanosoline produced.

FIG. **7** depicts the measurement of reticuline from the host cells shown in FIG. **5**.

FIG. **8** depicts the levels of substrate conversion obtained from host cells expressing different coding sequences available for the enzymes of the pathway. The data demonstrate that any combination of enzyme variants (obtained from different native host sources) will produce reticuline from the substrate. However, it is observed that certain combinations produce higher levels of reticuline than others.

FIG. **9** depicts measurement of levels of reticuline production when fed various amounts of the starting substrate.

FIG. **10** depicts measurement of levels of reticuline production from the supplied substrate at various points in the growth cycle of the host cells. The data demonstrate that the cells continue to produce and accumulate reticuline well into stationary phase, suggesting different fermentation strategies for maximizing reticuline production.

FIG. **11** depicts measurement of levels of reticuline production when the coding sequences for the heterologous enzymes are either integrated into the genome or expressed from plasmids. The data demonstrate that integration does not affect the level of accumulation of the desired BIA, confirming that the enzymes remain functional and expression is sufficient when integrated into the host genome.

FIG. **12** depicts the synthetic pathway present in embodiments of host cells in the present invention. Although the pathway may be longer, starting from tyrosine or norlaudanosoline as shown in other figures, this particular pathway begins with reticuline and ends with either laudanine or canadine. The pathway can include fewer enzymes than those displayed if the desired end result is one of the intermediates in the norlaudanosoline→canadine pathway.

FIGS. **13**A-**13**D depict the measurement of intermediates in the reticuline→canadine pathway. FIG. **13**A shows the level of canadine produced, FIG. **13**B shows the level of tetrahydrocolumbamine produced, FIG. **13**C shows the level of scoulerine produced, and FIG. **13**D shows the level of reticuline produced. Characteristic MS/MS fragmentation patterns are also shown for each ion.

FIG. **14** depicts a synthetic pathway from reticuline to thebaine. Note that the conversion of salutaridinol-7-O-acetate to thebaine is spontaneous, thus not requiring additional enzymatic steps.

FIG. **15** depicts salutaridine production in host cells comprising heterologous sequences coding for 6OMT, CNMT, 4'OMT, yCPR1 and yCYP2D6. The pathway synthesizes salutaridine when the cells are fed laudanosoline. The characteristic MS/MS fragmentation pattern is also shown for this ion.

FIGS. **16**A-**16**J depict exemplary combination and subcombination pathways of the present invention. FIGS. **16**A-**16**C depict exemplary overall combination pathways and FIGS. **16**D-**16**I depict the subcombination pathways including the chemical species and enzymes involved in the pathways. Pathway designations in FIGS. **16**D-**16**I refer to the pathway designations in FIGS. **16**A-**16**C. FIG. **16**J is but one embodiment of the methods of the present invention that combines a few of the subcombination pathways to produce a BIA.

## DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to compositions and methods for producing benzylisoquinoline alkaloids (BIAs). In particular, the invention relates to host cells that have been genetically engineered to express recombinant and/or have altered expression of endogenous enzymes involved in the biosynthesis of BIAs and their intermediates and derivatives.

In one embodiment, the cells of the present invention are non-plant cells. In a more particular embodiment, the cells are insect cells, mammalian cells, bacterial cells or yeast cells. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *Bacillus subtilis, Escherichia coli, Streptomyces* and *Salmonella typhimurium* cells and insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells. In one specific embodiment, the cells are yeast cells or *E. coli* cells. In a more specific embodiment, the yeast cells can be of the species *Saccharomyces cerevisiae* (*S. cerevisiae*). Yeast is also an ideal host cell because cytochrome P450 proteins, which are involved in certain steps in the synthetic pathways, are able to fold properly into the endoplasmic reticulum membrane so that activity is maintained, as opposed to bacterial cells which lack such intracellular compartments. Examples of yeast strains that can be used in the invention include, but are not limited to, S288C, W303, D273-10B, X2180, A364A, Σ1278B, AB972, SK1 and FL100. In specific examples, the yeast strain is any of S288C (MATα; SUC2 mal mel gal2 CUP1 flo2 flo8-1 hap1), BY4741 (MATa; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0), BY4742 (MATα; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0), BY4743 (MATa/MATα; his3Δ1/his3Δ1; leu2Δ0/leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ0; ura3Δ0/ura3Δ0), and WAT11 or W(R), derivatives of the W303-B strain (MATa; ade2-1; his3-11, -15; leu2-3, -112; ura3-1; canR; cyr+) which express the *Arabidopsis thaliana* NADPH-P450 reductase ATR1 and the yeast NADPH-P450 reductase CPR1, respectively. In another specific embodiment, the particular strain of yeast cell is W303α (MATα; his3-11,15 trp1-1 leu2-3 ura3-1 ade2-1), which is commercially available. The identity and genotype of additional examples of yeast strains can be found at EUROSCARF, available through the World Wide Web at web.uni-frankfurt.de/fb15/mikro/euroscarf/col_index.html.

Other example of cells that can serve as host cells are included, but not limited to, the strains listed in the table below.

TABLE I

| CSY | EUROSCARF/Open Biosystems Accession # | ORF deleted | Gene | Strain | Background |
|---|---|---|---|---|---|
| 3 | n/a | wild type | | | W303; Mat α; his3-11, 15 trp1-1 leu2-3 ura3-1 ade2-1 |
| 142 | n/a | YER073w/YPL061w | ALD5/ALD6 | | W303; Mat α; his3-11, 15 trp1-1 leu2-3 ura3-1 ade2-1 |
| 152 | Y10753 | YMR170c | ALD2 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |

TABLE I-continued

| CSY | EUROSCARF/Open Biosystems Accession # | ORF deleted | Gene | Strain | Background |
|---|---|---|---|---|---|
| 153 | Y10752 | YMR169c | ALD3 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 154 | Y11671 | YOR374w | ALD4 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 155 | Y10213 | YER073w | ALD5 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 156 | Y12767 | YPL061w | ALD6 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 157 | Y16510 | YML110c | COQ5 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 158 | Y16246 | YOL096c | COQ3 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 159 | Y13675 | YDR316w | OMS1 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 160 | 30701B | YGR001c | | CVDM003-01A | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 161 | Y11457 | YIL064w | | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 162 | Y15719 | YBR271w | | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 163 | B0006B | YJR129c | | CEN.EN2-1B | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 164 | B0199B | YNL024c | | CEN.HE27-2C | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 165 | Y12984 | YNL092w | | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 166 | Y12811 | YPL017c | | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 167 | Y12903 | YHR209w | | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 417 | 16236 | YOL086C | ADH1 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 418 | 10891 | YMR303C | ADH2 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 419 | 16217 | YMR083W | ADH3 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 420 | 14623 | YGL256W | ADH4 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 421 | 13284 | YBR145W | ADH5 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 422 | 16460 | YMR318C | ADH6 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 423 | 15821 | YCR105W | ADH7 | | BY4742; Mat α; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0; |
| 151 | Y10000 | wild type | | BY4742 | MATα; his3Δ1; leu2Δ0; lys2Δ0; ura3Δ0 |

The cells can be in any environment, provided the cells are able to express functional heterologous enzymes. In particular, the cells can be used in either in vitro or in vivo experiments. To be clear, in vitro, as used in the present invention, simply means outside of a living cell, regardless of the location of the cell. The term in vivo, on the other hand, indicates inside a cell, regardless of the location of the cell. In one embodiment, the cells are cultured under conditions that are conducive to enzyme expression and with appropriate substrates available to allow production of BIAs in vivo. Alternatively, the functional enzymes can be extracted from the host for production of BIAs under in vitro conditions. In another embodiment, the host cells can be placed back into a multicellular host organism. The host cells can be in any phase of growth, such as, but not limited to, stationary phase and log-growth phase, etc. In addition, the cultures themselves may be continuous cultures or they may be batch cultures.

The cell culture conditions for a particular cell type are well-known in the art and need not be repeated herein. In one particular embodiment, the host cells that comprise the various heterologous coding sequences can be cultured under standard or readily optimized conditions, with standard cell culture media and supplements. As one example, standard growth media when selective pressure for plasmid maintenance is not required may contain 20 g/L yeast extract, 10 g/L peptone, and 20 g/L dextrose (YPD). Host cells containing plasmids can be grown in synthetic complete (SC) media containing 1.7 g/L yeast nitrogen base, 5 g/L ammonium sulfate, and 20 g/L dextrose supplemented with the appropriate amino acids required for growth and selection. Alternative carbon sources which may be useful for inducible enzyme expression include sucrose, raffinose, and galactose. Cells can be grown at 30° C. with shaking at 200 rpm, typically in test tubes or flasks in volumes ranging from 1-1000 mL, or larger, in the laboratory. Culture volumes can also be scaled up for growth in larger fermentation vessels, for example, as part of an industrial process.

The term "host cells," as used in the present invention, are cells that harbor the heterologous coding sequences of the present invention. The heterologous coding sequences could be integrated stably into the genome of the host cells, or the heterologous coding sequences can be transiently inserted into the host cell. As used herein, the term "heterologous coding sequence" is used to indicate any polynucleotide that codes for, or ultimately codes for, a peptide or protein or its equivalent amino acid sequence, e.g., an enzyme, that is not normally present in the host organism and can be expressed in the host cell under proper conditions. As such, "heterologous coding sequences" includes additional copies of coding sequences that are normally present in the host cell, such that the cell is expressing additional copies of a coding sequence that are not normally present in the cells. The heterologous coding sequences can be RNA or any type thereof, e.g., mRNA, DNA or any type thereof, e.g., cDNA, or a hybrid of RNA/DNA. Examples of coding sequences include, but are not limited to, full-length transcription units that comprise such features as the coding sequence, introns, promoter regions, Y-UTRs and enhancer regions.

"Heterologous coding sequences" also includes the coding portion of the peptide or enzyme, i.e., the cDNA or mRNA sequence, of the peptide or enzyme, as well as the coding portion of the full-length transcriptional unit, i.e., the gene comprising introns and exons, as well as "codon optimized" sequences, truncated sequences or other forms of altered sequences that code for the enzyme or code for its equivalent amino acid sequence, provided that the equivalent amino acid sequence produces a functional protein. Such equivalent amino acid sequences can have a deletion of one or more amino acids, with the deletion being N-terminal, C-terminal or internal. Truncated forms are envisioned as long as they have the catalytic capability indicated herein. Fusions of two or more enzymes are also envisioned to facilitate the transfer of metabolites in the pathway, provided again that catalytic activities are maintained.

Operable fragments, mutants or truncated forms may be identified by modeling and/or screening. This is made possible by deletion of, for example, N-terminal, C-terminal or internal regions of the protein in a step-wise fashion, followed by analysis of the resulting derivative with regard to its activity for the desired reaction compared to the original sequence.

If the derivative in question operates in this capacity, it is considered to constitute an equivalent derivative of the enzyme proper.

Codon optimization is a well-known technique for optimizing the expression of heterologous polynucleotides in host cells and is reviewed in Gustafsson, C. et al., *Trends Biotechnol,* 22:346-353 (2004), which is incorporated by reference in its entirety.

The present invention also relates to heterologous coding sequences that code for amino acid sequences that are equivalent to the native amino acid sequences for the various enzymes. An amino acid sequence that is "equivalent" is defined as an amino acid sequence that is not identical to the specific amino acid sequence, but rather contains at least some amino acid changes (deletions, substitutions, inversions, insertions, etc.) that do not essentially affect the biological activity of the protein as compared to a similar activity of the specific amino acid sequence, when used for a desired purpose. The biological activity refers to, in the example of a decarboxylase, its catalytic activity. Equivalent sequences are also meant to include those which have been engineered and/or evolved to have properties different from the original amino acid sequence. Examples of mutable properties include catalytic activity, substrate specificity, selectivity, stability, solubility, localization, etc. In specific embodiments, an "equivalent" amino acid sequence contains at least 80%-99% identity at the amino acid level to the specific amino acid sequence, in particular at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94% and more in particular, at least 95%, 96%, 97%, 98% and 99% identity, at the amino acid level. In some cases, the amino acid sequence may be identical but the DNA sequence is altered such as to optimize codon usage for the host organism, for example.

The host cells may also be modified to possess one or more genetic alterations to accommodate the heterologous coding sequences. Alterations of the native host genome include, but are not limited to, modifying the genome to reduce or ablate expression of a specific enzyme that may interfere with the desired pathway. The presence of such native enzymes may rapidly convert one of the intermediates or final products of the pathway into a metabolite or other compound that is not usable in the desired pathway. Thus, if the activity of the native enzyme were reduced or altogether absent, the produced intermediates would be more readily available for incorporation into the desired product. For example, if the host cell is a yeast cell and the desired pathway produces 4-HPA from tyrosine, or a downstream metabolite thereof, it may be beneficial to reduce or ablate expression of the native endogenous alcohol and/or aldehyde dehydrogenase enzymes, which could convert the desired final product (4-HPA) into tyrosol or 4-hydroxyphenylacetic acid, respectively. Genetic alterations may also include modifying the promoters of endogenous genes to increase expression and/or introducing additional copies of endogenous genes. Examples of this include the construction/use of strains which overexpress the endogenous yeast NADPH-P450 reductase CPR1 to increase activity of heterologous P450 enzymes. In addition, endogenous enzymes such as ARO8, 9, and 10, which are directly involved in the synthesis of intermediate metabolites, may also be overexpressed.

The heterologous coding sequences of the present invention are sequences that encode enzymes, either wild-type or equivalent sequences, that are normally responsible for the production of BIAs in plants. The enzymes for which the heterologous sequences will code can be any of the enzymes in the BIA pathway, and can be from any known source. For example, Norcoclaurine synthase (NCS; EC 4.2.1.78) is found in at least *Thalictrum flavum, Papaver somniferum*, and *Coptis japonica* and is known to catalyze the condensation reaction of dopamine and 4-hydroxyphenylacetaldehyde (4-HPA) to form the trihydroxylated alkaloid (S)-norcoclaurine, which is widely accepted as the first "committed" step in the production of BIAs in plants. The choice and number of enzymes encoded by the heterologous coding sequences for the particular synthetic pathway should be chosen based upon the desired product. For example, the host cells of the present invention may comprise at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more heterologous coding sequences.

With regard to the heterologous coding sequences, the sequences are as reported in GENBANK unless otherwise noted. For example, the codon-optimized CYP2D6 sequence is included for reference along with the human monoamine oxidase A sequence with the first 10 amino acids optimized to facilitate translation initiation and proper folding in yeast.

A non-exhaustive list of enzymes that are contemplated in the present invention is shown in the table below. The host cells of the present invention may comprise any combination of the listed enzymes, from any source. Unless otherwise indicated, Accession numbers in Table I refer to GenBank. Some accession numbers refer to the *Saccharomyces* genome database (SGD) which is available on the world-wide web at www.yeastgenome.org.

TABLE II

| Enzyme Name | Abbrev. | Example Source Organism (Accession #) | Reference | Catalyzed Reactions |
|---|---|---|---|---|
| L-tyrosine/dopa decarboxylase 1 | TYDC1 | *P. somniferum* U08597 *T. flavum* AF314150 | Facchini, P. J. and De Luca, V. *J. Biol. Chem.* 269 (43), 26684-26690 (1994). PUBMED 7929401 | L-tyrosine-→L-tyramine, L-dopa→L-dopamine |
| L-tyrosine/dopa decarboxylase 2 | TYDC2 | *P. somniferum* U08598 *V. vinifera* AM429650 | Facchini, P. J. and De Luca, V. *J. Biol. Chem.* 269 (43), 26684-26690 (1994). PUBMED 7929401 | L-tyrosine-→L-tyramine, L-dopa→L-dopamine |
| Cytochrome P450 2D6 | CYP2D6 | *H. sapiens* NM000106 *S. cerevisiae* codon-optimized | Hiroi, T, Imaoka, S, and Funae, Y. *Biochem Biophys Res Commun.* 1998 Aug. 28; 249(3): 838-43. PUBMED 9731223 Zhu, W et. Al. *The* | L-tyramine→L-dopamine (R)-reticuline→(R)-salutaridine codeine→morphine |

TABLE II-continued

| Enzyme Name | Abbrev. | Example Source Organism (Accession #) | Reference | Catalyzed Reactions |
|---|---|---|---|---|
| | | | *Journal of Immunology*. Vol. 175, pp. 7357-7362 (2005). | |
| NADPH p450 reductase | CPR1 | *S. cerevisiae* SGDID: S000001084 | Turi, T G and Loper, J C. *J Biol Chem.* 1992 Jan. 25; 267(3): 2046-56. PUBMED 1730736 | L-tyramine-→L-dopamine (R)-reticuline→(R)-salutaridine codeine→morphine |
| Polyphenyloxidase | PPO | *A. bisporus* X85112, AJ223816 | Wichers, H J et. Al. *Appl. Microbiol. Biotechnol.* (2003) 61: 336-341. | L-tyrosine→L-dopa |
| Tyrosine hydroxylase | TyrH | *R. norvegicus* NM 012740 | Grima, B., Lamouroux, A., Blanot, F., Biguet, N. F. and Mallet, J. *Proc. Natl. Acad. Sci. U.S.A.* 82 (2), 617-621 (1985). PUBMED 2857492 | L-tyrosine→L-dopa |
| Tyrosine hydroxylase | TH2 | *H. sapiens* NM 000240 | Grima, B., Lamouroux, A., Boni, C., Julien, J. F., Javoy-Agid, F. and Mallet, J. *Nature* 326 (6114), 707-711 (1987). PUBMED 2882428 | L-tyrosine→L-dopa |
| GTPcyclohydrolase I | GTPCH1 | *H. sapiens* NM 00161 | Leff, S E et. al. *Experimental Neurology* 151, 249-64 (1998). | Produces $BH_4$ cofactor for tyrosine hydroxylase reaction L-tyrosine→L-dopa |
| Monoamine oxidase A | MaoA | *H. sapiens* J03792 | Bach, W J et. al. *Proc. Natl. Acad. Sci. USA*. Vol. 85, pp. 4934-4938, July 1988. | L-tyramine→4-HPA |
| Monoamine oxidase | maoA | *E. coli* D2367 | Azakami, H et. al. *J. Ferment. Bioeng.* 77, 315-319, 1994. | L-tyramine→4-HPA |
| Tyramine oxidase | tynA | *K. aerogenes* AB200269 | Cooper, R A. *FEMS Microbiol Lett.* 1997 Jan. 1; 146(1): 85-9. PUBMED 8997710 | L-tyramine→4-HPA |
| Aromatic amino acid transaminase | ARO8 | *S. cerevisiae* SGDID: S000003170 | Iraqui, I et. al. Mol. Gen. Genet. (1998) 257: 238-248. | L-tyrosine→4-hydroxyphenylpyruvate |
| Aromatic amino acid transaminase | ARO9 | *S. cerevisiae* SGDID: S000001179 | Iraqui, I et. al. Mol. Gen. Genet. (1998) 257: 238-248. | L-tyrosine→4-hydroxyphenylpyruvate |
| Phenylpyruvate decarboxylase | ARO10 | *S. cerevisiae* SGDID: S000002788 | Vuralhan, Z. et. al. *Appl. And Environ. Microbiol.* Vol. 71, No. 6, p. 3276-3284. | 4-hydroxyphenyl-pyruvate→4-HPA |
| Norcoclaurine synthase | NCS | *T. flavum*, AY376412 *P. somniferum* AY860500, AY860501 | Samanani, N, Liscombe, D K, and Facchini, P. *The Plant Journal* (2004) 40, 302-313. | L-dopamine + 4-HPA→ (S)-norcoclaurine |
| Norcoclaurine 6-O-methyltransferase | 6OMT | *T. flavum* AY61057 *P. somniferum* AY268894 | Ounaroon, A. et. al. *The Plant Journal* (2003) 36, 808-819. | (S)-norcoclaurine→ (S)-coclaurine norlaudanosoline→6-O-methyl norlaudanosoline laudanosoline→6-O-methyl laudanosoline |
| Coclaurine-N-methyltransferase | CNMT | *T. flavum* AY610508 *P. somniferum* AY217336 | Choi, Kum-Boo et. al. *J. Biol. Chem.* Vol. 277, No. 1, pp. 830-835, 2002. | coclaurine→ N-methylcoclaurine, laudanosoline→ N-methyl laudanosoline |
| Cytochrome P450 80B1 | CYP80B1 | *P. somniferum* AF191772 | Pauli, H H and Kutchan, T M. *Plant J.* 1998 March; 13(6): 793-801. | (S)-N-methylcoclaurine→ (S)-3'-hydroxy-N-methylcoclaurine |

TABLE II-continued

| Enzyme Name | Abbrev. | Example Source Organism (Accession #) | Reference | Catalyzed Reactions |
|---|---|---|---|---|
| 4'-O-methyltransferase | 4'OMT | *T. flavum* AY610510 *P. somniferum* AY217333, AY217334 | Morishige, T. et. al. *J. Biol. Chem.* Vol. 275, No. 30, pp. 23398-23405, 2000. | 3'-hydroxy-N-methylcoclaurine→reticuline norlaudanosoline→4'-O-methyl norlaudanosoline laudanosoline→4'-O-methyl laudanosoline |
| Berberine bridge enzyme | BBE | *P. somniferum* AF025430 | Facchini, P. J., Penzes, C., Johnson, A. G. and Bull, D. *Plant Physiol.* 112 (4), 1669-1677 (1996). PUBMED 8972604 | (S)-reticuline→(S)-scoulerine |
| Reticuline 7-O-methyltransferase | 7OMT | *P. somniferum* AY268893 | Ounaroon, A. et. al. *The Plant Journal* (2003) 36, 808-819. | reticuline→laudanine |
| Scoulerine 9-O-methyltransferase | S9OMT | *T. flavum* AY610512 | Samanani, N., Park, S. U. and Facchini, P. J. *Plant Cell* 17 (3), 915-926 (2005). PUBMED 15722473 | (S)-scoulerine→(S)-tetrahydrocolumbamine |
| Canadine synthase | CYP719A | *T. flavum* AY610513 | Samanani, N., Park, S. U. and Facchini, P. J. *Plant Cell* 17 (3), 915-926 (2005). PUBMED 15722473 Ikezawa, N. et. al. *J. Biol. Chem.* Vol. 278, No. 40, pp. 38557-38565, 2003. | (S)tetrahydrocolumbamine→(S)-canadine |
| NADPH P450 reductase | ATR1 | *A. thaliana* NM 118585 | Louërat-Oriou B, Perret A, Pompon D. *Eur J Biochem.* 1998 Dec. 15; 258(3): 1040-9. | Reductase partner for cytochrome P450s Ex. (S)tetrahydro-columbamine→ (S)-canadine |
| Salutaridine reductase | SalR | *P. somniferum* DQ316261 | Ziegler, J. et. al. *Plant J.* 48 (2), 177-192 (2006) | salutaridine→salutaridinol |
| Salutaridinol 7-O-acetyltransferase | SalAT | *P. somniferum* AF339913 | Grothe, T., Lenz, R. and Kutchan, T. M. *J. Biol. Chem.* 276 (33), 30717-30723 (2001). PUBMED 11404355 | salutaridinol→salutaridinol-7-O-acetate→thebaine |
| Codeine reductase | COR | *P. somniferum* AF108432 | Unterlinner, B., Lenz, R. and Kutchan, T. M. *Plant J.* 18 (5), 465-475 (1999). PUBMED 1041769 | codeinone→codeine |
| Berbamunine synthase | CYP80A1 | *B. stolonifera* U09610 | Kraus, P F and Kutchan, T M. *Proc Natl Acad Sci USA.* 1995 Mar. 14; 92(6): 2071-5. | 2 (R)-N-methylcoclaurine→guattegaumerine (R)-N-methlcoclaurine + (S)-N-methylcoclaurine→berbamunine |

In one specific embodiment, the present invention relates to host cells that produce 4-Hydroxyphenylacetaldehyde (4-HPA) from tyrosine. For example, the host cells that produce 4-HPA from tyrosine comprise at least two heterologous coding sequences, wherein each of the heterologous coding sequences encodes a separate enzyme that is involved in the biosynthetic pathway that converts tyrosine to 4-HPA. In a more specific embodiment, the host cells that produce 4-HPA from tyrosine comprise L-tyrosine/dopa decarboxylase (TYDC, *P. somniferum*) and one of monoamine oxidase (maoA, *E. coli* or *Homo sapiens*) or Tyramine oxidase (tyn A, *Klebsiella aerogenes*). In another specific embodiment, the host cells that produce 4-HPA from tyrosine comprise Aromatic amino acid transaminase (ARO8/ARO9, *S. cerevisiae*) and Phenylpyruvate decarboxylase (ARO10, *S. cerevisiae*).

In another specific embodiment, the present invention relates to host cells that produce dopamine from tyrosine. For example, the host cells that produce dopamine comprise at least two heterologous coding sequences, wherein each of the heterologous coding sequences encodes a separate enzyme that is involved in the biosynthetic pathway that converts tyrosine to dopamine. In a more specific embodiment, the host cells that produce dopamine from tyrosine comprise a Tyrosine/dopa decarboxylase (TYDC, *P. somniferum*) and one of Cytochrome P450 2D6 (CYP2D6, *H. sapiens*) or Codon-Optimized Cytochrome P450 2D6 (CYP2D6, *S. cerevisiae*). To improve of the activity of CYP2D6, additional copies of the yeast NADPH-P450 reductase (yCPR1) may be expressed either from the chromosome or a plasmid. In another specific embodiment, the host cells that produce dopamine from tyrosine comprise a Tyrosine hydroxylase (PPO *Agaricus bisporus*; TH2, *H. sapiens*; TyrH, *Rattus norvegicus*) and Tyrosine/dopa decarboxylase (TYDC, *P. somniferum*).

In another specific embodiment, the present invention relates to host cells that convert tyrosine into norcoclaurine. Regardless of the source of the tyrosine starting material, the host cells of the present invention that produce norcoclaurine comprise at least three heterologous coding sequences, wherein each of the heterologous coding sequences encodes a separate enzyme, or its equivalent, that is involved in the biosynthetic pathway that converts tyrosine to norcoclaurine. In one specific embodiment, the host cells that produce norcoclaurine from tyrosine comprise the L-tyrosine/dopa decarboxylase (TYDC, *P. somniferum*), Monoamine oxidase (MaoA, *E. coli*), one of Cytochrome P450 2D6 (CYP2D6, *H. sapiens*) or Codon-Optimized Cytochrome P450 2D6 (CYP2D6, *S. cerevisiae*), and NCS (*T. Flavum* or *P. somniferum*) coding sequences. To improve the activity of CYP2D6, additional copies of the endogenous yeast P450 NADPH reductase (yCPR1) may be expressed either from the chromosome or a plasmid. Of course, the embodiment above may further comprise additional heterologous coding sequences that will continue the synthetic pathway to create at least one additional metabolite. For example, the presence of the heterologous coding sequence that codes for Norcoclaurine 6-O-methyltransferase (6OMT, *T. flavum, P. somniferum*) will further metabolize norcoclaurine into coclaurine. Other pathways to/from norcoclaurine are depicted herein.

The embodiment above can serve as the basis of additional embodiments. For example, embodiments comprising TYDC, CYP2D6, maoA, NCS, 6OMT may further comprise the Coclaurine-N-methyltransferase (CNIVIT, *T. flavum, P. somniferum*) heterologous coding sequence, the embodiments of which may further comprise the Cytochrome P450 80B1 (CYP80B1, *P. somniferum*) heterologous coding sequence, the embodiments of which may further comprise the 4'-O-methyltransferase (4'OMT, *T. flavum, P. somniferum*) heterologous coding sequence, the embodiments of which may further comprise Berberine bridge enzyme (BBE, *P. somniferum*), etc. The embodiments in which the host cell comprises TYDC, CYP2D6, maoA, NCS, 6OMT and CNMT will generate N-methylcoclaurine ultimately from tyrosine. The embodiments in which the host cell comprises TYDC, CYP2D6, maoA, NCS, 6OMT, CNMT and CYP80B1 will generate 3'-Hydroxy-N-methylcoclaurine ultimately from tyrosine. The embodiments in which the host cell comprises TYDC, CYP2D6, maoA, NCS, 6OMT, CNMT CYP80B1 and 4'OMT will generate reticuline ultimately from tyrosine. The embodiments in which the host cell comprises TYDC, CYP2D6, maoA, NCS, 6OMT, CNMT CYP80B1, 4'OMT and BBE will generate scoulerine ultimately from tyrosine. All strains containing either CYP2D6 and/or CYP80B1 will likely require overexpression of CPR1 and/or ATR1 NADPH-P450 reductases for optimal activity.

Of course, the desired pathways need not start with tyrosine. For example, the synthetic pathways generated in the host cells may start with laudanosoline, methyl laudanosoline, norlaudanosoline, methyl norlaudanosoline, or another compound that may or may not be normally present in the endogenous BIA pathway. Thus, the starting material may be non-naturally occurring or the starting material may be naturally occurring. Additional examples of starting material include, but are not limited to, tyramine, dopamine, 4-HPA, 4-HPPA, norcoclaurine, coclaurine, N-methylcoclaurine, 3'-hydroxy-N-methylcoclaurine, reticuline, scoulerine, tetrahydrocolumbamine, canadine, laudanine, sanguinarine, morphine, codeine, codeinone and dimethyl tetrahydoisoquinoline, e.g., 6,7-dimethyl-1-2-3-4-tetrahydroisoquinoline. Other compounds may also be used as the starting material in the desired synthetic pathway and one of skill in the art would recognize the necessary starting material, based upon the synthetic pathway present in the host cell. The source of the starting material may be from the host cell itself, e.g., tyrosine, or the starting material may be added or supplemented to the host cell from an outside source. For example, if the host cells are growing in liquid culture (an in vivo environment), the cell media may be supplemented with the starting material, e.g., tyrosine or norlaudanosoline, which is transported into the cells and converted into the desired products.

In one embodiment, the host cells of the claimed invention convert norlaudanosoline into reticuline. The norlaudanosoline may be generated through a normal or synthetic pathway in the same or different host cell, or the norlaudanosoline may be fed to the cells from the outside. In this particular embodiment, the host cells comprise 6OMT, CNMT and 4'OMT. This embodiment can serve as the basis of additional embodiments. For example, embodiments comprising 6OMT, CNMT and 4'OMT may further comprise BBE or Reticuline 7-O-methyltransferase (7OMT, *P. somniferum*) the embodiments of which may further comprise Scoulerine 9-O-methyltransferase (S9OMT, *T. flavum*), the embodiments of which may further comprise Canadine synthase (CYP719A, *T. flavum*). The embodiments that comprise 6OMT, CNMT and 4'OMT will generate reticuline from norlaudansoline. The embodiments that comprise 6OMT, CNMT, 4'OMT and BBE will generate scoulerine from norlaudanosoline. The embodiments that comprise 6OMT, CNMT, 4'OMT, and CYP2D6 with its reductase partner (CPR1 or ATR1) will generate salutaridine from norlaudanosoline. The embodiments that comprise 6OMT, CNMT, 4'OMT and 7OMT will generate laudanine from norlaudanosoline. The embodiments that comprise 6OMT, CNMT, 4'OMT, BBE and S9OMT will generate tetrahydrocolumbamine from norlaudanosoline. The embodiments that comprise 6OMT, CNMT, 4'OMT, BBE, S9OMT and CYP719A with its reductase partner ATR1 will generate canadine from norlaudanosoline.

The following is a non-exhaustive list of exemplary host organisms comprising heterologous coding sequences. The list is not intended to limit the scope of the invention in any way.

TABLE III

| Strain | Background | Plasmid(s) | Enzyme(s) |
|---|---|---|---|
| CSY73 | W303α | | $P_{ARO9}$::TEF, $P_{ARO10}$::TEF |
| CSY87 | W303α | pCS251 | $P_{TEF1}$-AbPPO2 |
| CSY88 | W303α | pCS251, pCS221 | $P_{TEF1}$-AbPPO2, $P_{TEF1}$-TYDC2 |
| CSY94 | W303α | pCS250, pCS283 | $P_{TEF1}$-TfNCSΔ10, $P_{TEF1}$-TYDC2, $P_{TEF1}$-maoA |
| CSY95 | W303α | | ChrIV 122460::$P_{TEF1}$-TYDC2 |

TABLE III-continued

| Strain | Background | Plasmid(s) | Enzyme(s) |
|---|---|---|---|
| CSY104 | CSY95 | | ChrV 1100::$P_{TEF1}$-maoA |
| CSY107 | W303α | pCS222, pCS330 | $P_{tetO7}$-yCPR1, $P_{TEF1}$-TYDC2, $P_{TEF1}$-yCYP2D6 |
| CSY116 | CSY104 | | his3::$P_{GPD}$-yCPR1 |
| CSY176 | W303α | | his3::$P_{GAL1}$-TfNCS |
| CSY177 | W303α | | his3::$P_{GAL1}$-Tf6OMT |
| CSY178 | W303α | | his3::$P_{GAL1}$-PsNCS2 |
| CSY179 | W303α | | his3::$P_{GAL1}$-Ps6OMT |
| CSY234 | CSY194 W(R) | pCS330 | $P_{TEF1}$-TYDC2, $P_{TEF1}$-yCYP2D6 |
| CSY235 | CSY194 W(R) | pCS222, pCS330 | $P_{tetO7}$-yCPR1, $P_{TEF1}$-TYDC2, $P_{TEF1}$-yCYP2D6 |
| CSY307 | W303α | pCS827, pCS830 | $P_{TEF1}$-Ps6OMT, $P_{TEF1}$-PsCNMT, $P_{TEF1}$-Ps4'OMT |
| CSY308 | W303α | pCS828, pCS830 | $P_{TEF1}$-Ps6OMT, $P_{TEF1}$-TfCNMT, $P_{TEF1}$-Ps4'OMT |
| CSY309 | W303α | pCS829, pCS830 | $P_{TEF1}$-Tf6OMT, $P_{TEF1}$-PsCNMT, $P_{TEF1}$-Ps4'OMT |
| CSY310 | W303α | pCS772, pCS830 | $P_{TEF1}$-Tf6OMT, $P_{TEF1}$-TfCNMT, $P_{TEF1}$-Ps4'OMT |
| CSY311 | W303α | pCS827, pCS831 | $P_{TEF1}$-Ps6OMT, $P_{TEF1}$-PsCNMT, $P_{TEF1}$-Tf4'OMT |
| CSY312 | W303α | pCS828, pCS831 | $P_{TEF1}$-Ps6OMT, $P_{TEF1}$-TfCNMT, $P_{TEF1}$-Tf4'OMT |
| CSY313 | W303α | pCS829, pCS831 | $P_{TEF1}$-Tf6OMT, $P_{TEF1}$-PsCNMT, $P_{TEF1}$-Tf4'OMT |
| CSY314 | W303α | pCS772, pCS831 | $P_{TEF1}$-Tf6OMT, $P_{TEF1}$-TfCNMT, $P_{TEF1}$-Tf4'OMT |
| CSY288 | W303α | | his3::$P_{TEF1}$-Ps6OMT, leu2::$P_{TEF1}$-PsCNMT, ura3::$P_{TEF1}$-Ps4'OMT |
| CSY334 | W303α | | his3::$P_{TEF1}$-Ps6OMT, leu2::$P_{TEF1}$-PsCNMT, ura3::$P_{TEF1}$-Tf4'OMT |
| CSY316 | W303α | | his3::$P_{GAL1}$-Ps6OMT-loxP-KanR, leu2::$P_{TEF1}$-PsCNMT, ura3::$P_{TEF1}$-Ps4'OMT |
| CSY317 | W303α | | his3::$P_{TEF1}$-Ps6OMT, leu2::$P_{GAL1}$-PsCNMT-loxP-URA3, ura3::$P_{TEF1}$-Ps4'OMT |
| CSY318 | W303α | | his3::$P_{TEF1}$-Ps6OMT, leu2::$P_{TEF1}$-PsCNMT, ura3::$P_{GAL1}$-Ps4'OMT-loxP-LEU2 |
| CSY319 | W303α | | his3::$P_{TEF1}$-Ps6OMT, leu2::$P_{TEF1}$-PsCNMT, ura3::$P_{GAL1}$-Tf4'OMT-loxP-LEU2 |
| CSY325 | W303α | | his3::$P_{GAL1}$-Ps6OMT-loxP-KanR, leu2::$P_{TEF1}$-PsCNMT, ura3::$P_{TEF1}$-Ps4'OMT, gal2::HIS3 |
| CSY326 | W303α | | his3::$P_{TEF1}$-Ps6OMT, leu2::$P_{GAL1}$-PsCNMT-loxP-URA3, ura3::$P_{TEF1}$-Ps4'OMT, gal2::HIS3 |
| CSY327 | W303α | | his3::$P_{TEF1}$-Ps6OMT, leu2::$P_{TEF1}$-PsCNMT, ura3::$P_{GAL1}$-Ps4'OMT-loxP-LEU2, gal2::HIS3 |
| CSY328 | W303α | | his3::$P_{TEF1}$-Ps6OMT, leu2::$P_{TEF1}$-PsCNMT, ura3::$P_{GAL1}$-Tf4'OMT-loxP-LEU2, gal2::HIS3 |
| CSY336 | CSY288 | pCS1018 | $P_{TEF1}$-PsBBE |
| CSY337 | CSY288 | pCS1070 | $P_{TEF1}$-PsBBE, $P_{TEF1}$-TfS9OMT |
| CSY338 | CSY334 | pCS1018 | $P_{TEF1}$-PsBBE |
| CSY339 | CSY334 | pCS1070 | $P_{TEF1}$-PsBBE, $P_{TEF1}$-TfS9OMT |
| CSY399 | CSY288 | pCS1018, pCS953, pCS1058 | $P_{TEF1}$-PsBBE, $P_{TEF1}$-TfS9OMT, $P_{TEF1}$-TfCYP719A, $P_{TEF1}$-AtATR1 |
| CSY400 | CSY334 | pCS1018, pCS953, pCS1058 | $P_{TEF1}$-PsBBE, $P_{TEF1}$-TfS9OMT, $P_{TEF1}$-TfCYP719A, $P_{TEF1}$-AtATR1 |
| CSY401 | CSY288 | pCS1163 | $P_{TEF1}$-PsR7OMT |
| CSY402 | CSY334 | pCS1163 | $P_{TEF1}$-PsR7OMT |
| CSY409 | CSY334 | | his3::$P_{TEF1}$-Ps6OMT, leu2::$P_{TEF1}$-PsCNMT, ura3::$P_{TEF1}$-Tf4'OMT, trp1::$P_{TEF1}$-AtATR1(KanR) |
| CSY410 | CSY409 | pCS1018, pCS953 | $P_{TEF1}$-PsBBE, $P_{TEF1}$-TfS9OMT, $P_{TEF1}$-TfCYP719A |
| CSY424 | CSY334 | pCS782 | $P_{TEF1}$-yCYP2D6 |
| CSY425 | CSY409 | pCS782 | $P_{TEF1}$-yCYP2D6 |
| CSY426 | CSY288 | | trp1::$P_{TEF1}$-yCPR1(KanR) |
| CSY427 | CSY426 | pCS782 | $P_{TEF1}$-yCYP2D6 |

The promoters driving expression of the heterologous coding sequences can be constitutive promoters or inducible promoters, provided that the promoters can be active in the host cells. The heterologous coding sequences may be expressed from their native promoters, or non-native promoters may be used. Although not a requirement, such promoters should be medium to high strength in the host in which they are used. Promoters may be regulated or constitutive. In one embodiment, promoters that are not glucose repressed, or repressed only mildly by the presence of glucose in the culture medium, should be used. There are numerous suitable promoters, examples of which include promoters of glycolytic genes such as the promoter of the *B. subtilis* tsr gene (encoding fructose biphosphate aldolase) or GAPDH promoter from yeast *S. cerevisiae* (coding for glyceraldehyde-phosphate dehydrogenase) (Bitter G. A., Meth. Enzymol. 152:673 684 (1987)). Other Strong Promoters Include the ADHI Promoter of baker's yeast (Ruohonen L., et al., *J. Biotechnol.* 39:193 203 (1995)), the phosphate-starvation induced promoters such as the PHOS promoter of yeast (Hinnen, A., et al., in *Yeast Genetic Engineering*, Barr, P. J., et al. eds, Butterworths (1989), and the alkaline phosphatase promoter from *B. licheniformis* (Lee. J. W. K., et al., *J. Gen. Microbiol.* 137:1127 1133 (1991)). Some specific examples of yeast promoters include inducible promoters such as Gall-10, Gall, GalL, GalS, repressible promoter Met25, tetO, and constitutive promoters such as glyceraldehyde 3-phosphate dehydrogenase promoter (GPD), alcohol dehydrogenase promoter (ADH), translation-elongation factor-1-alpha promoter (TEF), cytochrome c-oxidase promoter (CYC1), MRP7 promoter, etc. Autonomously replicating yeast expression vectors containing promoters inducible by hormones such as glucocorticoids, steroids, and thyroid hormones are also known and include, but are not limited to, the glucorticoid responsive element (GRE) and thyroid hormone responsive element (TRE). These and other examples are described U.S. Pat. No. 7,045,290, which is incorporated by reference, including the references cited therein. Additional vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. Additionally any promoter/enhancer combination (as per the Eukaryotic Promoter Data Base EPDB) could also be used to drive expression of genes. Similarly, one of skill in the art can choose appropriate promoters specific to the host cell, e.g., *E. coli*. One can also use promoter selection to optimize transcript, and hence, enzyme levels to maximize production while minimizing energy resources.

Vectors useful in the present invention include vectors for use in yeast and other cells. Yeast vectors can be broken up into 4 general categories: integrative vectors (YIp), autonomously replicating high copy-number vectors (YEp), autonomously replicating low copy-number vectors (YCp) and vectors for cloning large fragments (YACs). There are myriad of yeast expression vectors that are commercially available from sources such as, but not limited to, American Type Culture Collection (ATCC, Manassas, Va., USA) and Invitrogen Corp. (Carlsbad, Calif., USA).

Alternatively, insect cells may be used as host cells. In one embodiment, the polypeptides of the invention are expressed using a baculovirus expression system (see, Luckow et al., Bio/Technology, 1988, 6, 47; BACULOVIRUS EXPRESSION VECTORS: A LABORATORY MANUAL, O'Rielly et al. (Eds.), W.H. Freeman and Company, New York, 1992; and U.S. Pat. No. 4,879,236, each of which is incorporated herein by reference in its entirety). In addition, the MAXBAC™ complete baculovirus expression system (Invitrogen) can, for example, be used for production in insect cells.

Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated in vitro, for example using T7 promoter regulatory sequences and T7 polymerase.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, et al (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin, dihydrofolate reductase (DHFR) and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding the functional enzyme, or its equivalent, or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die).

Similarly, if the host cells are bacterial cells or animal or insect cells, there are a variety of commercially available expression vectors from which to choose. The choice of expression vector system will be apparent to one of skill in the art. One example of a yeast expression vector includes, but is not limited to, p413-TEF, p426-GPD, pCM190, pRS313, pYES2-NT/A, etc.

The choice of yeast plasmids will depend on the host. For *Z. rouxii* vectors based on the native cryptic plasmids pSR1 (Toh, E. et al., *J. Bacteriol.* 151:1380-1390 (1982)), pSB1, pSB2, pSB3 or pSB4 (Toh-E et al., *J. Gen. Microbial.* 130: 2527-2534 (1984)) may be used. Plasmid pSRT303D (Jearnpipatkul, A., et al., *Mol. Gen. Genet.* 206:88-94 (1987)) is an example of useful plasmid vector for *Zygosaccharomyces* yeast.

Methods of transforming yeast for the purposes of the present invention are well known in the art. Briefly, inserting DNA into yeast can be accomplished with techniques that include but are not limited to, those using spheroplasts, treating with lithium salts and electroporation. The methods are used to insert the heterologous coding sequences into the host cells such that the host cells will functionally express the enzymes or their equivalents and convert the starting/intermediate compounds into the desired end product.

Of course, the present invention also relates to methods of producing BIAs comprising culturing the host cells under conditions suitable for protein production such that the heterologous coding sequences are expressed in the host cells and act upon the starting/intermediate molecules.

In another embodiment of the present invention the host cells may also be used for functional genomics studies in both plant and animals. For example, host cells that are able to convert a given substrate such as norlaudanosoline into reticuline or other downstream BIAs can be used to screen libraries of plant cDNA sequences to discover enzymes which act on the product molecule. Of course, the screening methods can also be applied to precursors of BIAs. The screening methods can be accomplished by cloning a cDNA library from an organism, such as a plant or any organism that produces BIAs or an intermediate thereof, e.g., dopamine, into a suitable expression vector, e.g., a yeast expression vector, and transforming the library of plasmids into the engineered host cells. The standard LiAc/SSD/PEG method can be used. Single colonies can then be grown in liquid culture in the presence of substrate and the growth media or cell extract analyzed by LC-MS. New BIA molecules and the corresponding enzymes catalyzing their production can be identified by chromatogram peaks not present in strains lacking the cDNA library sequence. In vitro or other high-throughput methods can also be used if a suitable assay has been developed for a particular metabolite or byproduct, for example. An additional area of study where these engineered host cells can be employed is in the characterization of the recombinant enzymes known or suspected to be involved in these pathways. In particular, host cells expressing one or more heterologous coding sequences can be grown in the presence of various substrates and the resulting metabolites analyzed by LC-MS or other methods. Both in vivo and in vitro methods can be used in this manner to determine the substrate specificities of these enzymes and possibly discover new catalytic activities.

## EXAMPLES

### Example 1

### Construction of Yeast Expression Vectors

Standard molecular biology methods were used to construct the yeast expression vectors. Heterologous coding sequences for the genes of interest were received as plasmids, typically suited for expression in *E. coli*. Coding sequences were either amplified by polymerase chain reaction (PCR) or excised from the vectors if restriction sites were compatible with the destination vector. Briefly, yeast shuttle vectors were constructed based on pCM185 and pCM180 which have an ampicillin resistance marker for maintenance in *E. coli*, URA and TRP selection markers, respectively, and a centromeric (ARS1/CEN4) origin of replication for yeast. To construct exemplary vectors, the TEF1 promoter was amplified from p413-TEF and the CYC1 promoter from pCM190 and assembled with the NCS coding sequence using PCR methods. Primers for each segment included suitable restriction sites both for cloning into the plasmid backbone and allowing the coding sequence to be easily replaced. This promoter-gene-terminator assembled PCR product was cloned into XhoI/BamHI sites of pCM185. Similar methods were used to make a second DNA insert containing the TEF promoter and 6OMT gene, which was then cloned into PmeI/NotI sites of the previous vector such that a CYC1 terminator for this gene was included on the plasmid backbone. Similar methods were used to construct the analogous vector with a TRP selection marker. In later constructs, the origin of replication was replaced with the 2μ origin using standard cloning procedures to allow for high copy expression in yeast. For cloning and expression of desired enzyme combinations, heterologous coding sequences were cloned into these primary vectors; restriction sites were changed using site-directed mutagenesis if necessary. To remove the second gene from these constructs, vectors were digested with MluI and self-ligated. To remove the first gene from these constructs, the vectors were digested with XhoI and either BamHI or PmeI, ends were blunted using the Klenow enzyme, and self-ligated. Alternatively, a single promoter vector can be made by cloning the gene of interest between the first promoter and second terminator. Analogous vectors with the HIS selection marker were also constructed as needed; for example, to express more than four heterologous coding sequences.

## Example 2

### Production of Codon-Optimized CYP2D6

The coding sequence for CYP2D6 was optimized based on codon usage in *S. cerevisiae* as well as RNA secondary structure, using commercially available service providers, such as DNA2.0 Inc. (Menlo Park, Calif., USA). There are other service providers that offer codon-optimized sequences, and some algorithms are available on the world-wide web.

The following is an example of a sequence for yeast codon-optimized CYP2D6 sequence; SalI and NotI restriction sites for cloning are underlined.

```
   1 GTCGACATGG CATTGGAAGC ACTAGTCCCT TTAGCTGTAA TTGTAGCAAT
  51 ATTCCTGTTA TTGGTAGACC TTATGCATAG AAGACAAAGA TGGGCTGCAA
 101 GATACCCACC CGGCCCACTA CCCTTGCCAG GACTAGGTAA CCTTTTACAT
 151 GTTGATTTCC AAAATACTCC GTACTGTTTT GATCAATTGA GGAGAAGATT
 201 CGGAGATGTT TTCAGTCTGC AGTTGGCATG GACACCAGTC GTCGTTTTAA
 251 ATGGTTTGGC TGCAGTAAGA GAAGCTTTAG TTACGCATGG CGAAGATACG
 301 GCGGACAGGC CTCCTGTGCC CATTACACAG ATATTGGGTT TCGGACCTAG
 351 ATCTCAGGGT GTATTCCTTG CCCGTTACGG TCCTGCGTGG AGAGAACAGA
 401 GAAGGTTTTC TGTATCAACA CTTAGGAATT TGGGTCTAGG CAAGAAATCA
 451 TTGGAACAAT GGGTGACCGA GGAAGCCGCT TGTTTGTGCG CAGCCTTTGC
 501 TAATCATTCT GGCCGTCCTT TTAGACCTAA TGGATTACTT GATAAAGCAG
 551 TATCTAATGT GATTGCCTCC TTAACATGTG GTAGACGTTT TGAGTACGAT
 601 GACCCAAGGT TTTTGAGATT GTTAGATCTA GCACAAGAGG GATTAAAGGA
 651 AGAAAGTGGT TTCTTGAGAG AGGTTTTGAA TGCTGTTCCA GTGCTATTAC
 701 ACATTCCAGC CCTAGCTGGA AAGGTCTTGA GATTTCAAAA GGCTTTCTTA
 751 ACGCAGCTTG ATGAGTTACT TACAGAGCAT AGGATGACTT GGGATCCTGC
 801 TCAACCCCCG AGAGATCTAA CCGAGGCCTT CCTGGCTGAA ATGGAAAAAG
 851 CAAAGGGTAA TCCGGAAAGT TCCTTCAATG ATGAAAACCT GAGAATTGTC
 901 GTGGCGGACT TGTTCTCTGC CGGAATGGTG ACAACGTCTA CTACTTTGGC
 951 CTGGGGACTT CTATTAATGA TTCTTCATCC AGACGTCCAG AGAAGAGTGC
1001 AACAAGAAAT AGATGATGTG ATAGGACAAG TTAGAAGGCC AGAAATGGGT
1051 GACCAGGCAC ATATGCCATA TACGACTGCT GTAATCCATG AAGTGCAACG
1101 TTTTGGGGAC ATTGTCCCCT TGGGAATGAC CCACATGACT TCTCGTGATA
1151 TTGAAGTACA AGGTTTCAGA ATACCAAAGG GAACTACGCT GATTACGAAT
1201 CTGTCTAGCG TGCTAAAAGA CGAAGCTGTC TGGGAGAAGC CATTTAGGTT
1251 TCATCCAGAA CACTTCTTAG ACGCTCAGGG TCATTTCGTA AAGCCTGAAG
1301 CATTCCTTCC GTTTAGTGCC GGACGTAGGG CGTGTTTGGG TGAACCATTA
```

-continued

```
1351 GCTAGAATGG AATTATTCCT TTTTTTTACA TCTTTATTGC AGCACTTTTC

1401 ATTTTCTGTT CCGACTGGCC AACCCAGACC TAGCCATCAT GGTGTTTTTG

1451 CTTTCCTAGT TTCTCCCTCT CCTTATGAAT TATGCGCGGT TCCCCGTTGA

1501 GCGGCCGC
```

The following is an example of human MAO A sequence optimized for expression in yeast and includes 8 nt preceding the start codon, which is underlined:

```
   1 AATTAATAAT GGAAAACCAA GAAAAGGCTT CTATCGCGGG CCACATGTTC

  51 GACGTAGTCG TGATCGGAGG TGGCATTTCA GGACTATCTG CTGCCAAACT

 101 CTTGACTGAA TATGGCGTTA GTGTTTTGGT TTTAGAAGCT CGGGACAGGG

 151 TTGGAGGAAG AACATATACT ATAAGGAATG AGCATGTTGA TTACGTAGAT

 201 GTTGGTGGAG CTTATGTGGG ACCAACCCAA AACAGAATCT TACGCTTGTC

 251 TAAGGAGCTG GGCATAGAGA CTTACAAAGT GAATGTCAGT GAGCGTCTCG

 301 TTCAATATGT CAAGGGGAAA ACATATCCAT TTCGGGGCGC CTTTCCACCA

 351 GTATGGAATC CCATTGCATA TTTGGATTAC AATAATCTGT GGAGGACAAT

 401 AGATAACATG GGGAAGGAGA TTCCAACTGA TGCACCCTGG GAGGCTCAAC

 451 ATGCTGACAA ATGGGACAAA ATGACCATGA AAGAGCTCAT TGACAAAATC

 501 TGCTGGACAA AGACTGCTAG GCGGTTTGCT TATCTTTTTG TGAATATCAA

 551 TGTGACCTCT GAGCCTCACG AAGTGTCTGC CCTGTGGTTC TTGTGGTATG

 601 TGAAGCAGTG CGGGGGCACC ACTCGGATAT TCTCTGTCAC CAATGGTGGC

 651 CAGGAACGGA AGTTTGTAGG TGGATCTGGT CAAGTGAGCG AACGGATAAT

 701 GGACCTCCTC GGAGACCAAG TGAAGCTGAA CCATCCTGTC ACTCACGTTG

 751 ACCAGTCAAG TGACAACATC ATCATAGAGA CGCTGAACCA TGAACATTAT

 801 GAGTGCAAAT ACGTAATTAA TGCGATCCCT CCGACCTTGA CTGCCAAGAT

 851 TCACTTCAGA CCAGAGCTTC CAGCAGAGAG AAACCAGTTA ATTCAGCGGC

 901 TTCCAATGGG AGCTGTCATT AAGTGCATGA TGTATTACAA GGAGGCCTTC

 951 TGGAAGAAGA AGGATTACTG TGGCTGCATG ATCATTGAAG ATGAAGATGC

1001 TCCAATTTCA ATAACCTTGG ATGACACCAA GCCAGATGGG TCACTGCCTG

1051 CCATCATGGG CTTCATTCTT GCCCGGAAAG CTGATCGACT TGCTAAGCTA

1101 CATAAGGAAA TAAGGAAGAA GAAAATCTGT GAGCTCTATG CCAAAGTGCT

1151 GGGATCCCAA GAAGCTTTAC ATCCAGTGCA TTATGAAGAG AAGAACTGGT

1201 GTGAGGAGCA GTACTCTGGG GGCTGCTACA CGGCCTACTT CCCTCCTGGG

1251 ATCATGACTC AATATGGAAG GGTGATTCGT CAACCCGTGG GCAGGATTTT

1301 CTTTGCGGGC ACAGAGACTG CCACAAAGTG GAGCGGCTAC ATGGAAGGGG

1351 CAGTTGAGGC TGGAGAACGA GCAGCTAGGG AGGTCTTAAA TGGTCTCGGG

1401 AAGGTGACCG AGAAAGATAT CTGGGTACAA GAACCTGAAT CAAAGGACGT

1451 TCCAGCGGTA GAAATCACCC ACACCTTCTG GGAAAGGAAC CTGCCCTCTG

1501 TTTCTGGCCT GCTGAAGATC ATTGGATTTT CCACATCAGT AACTGCCCTG

1551 GGGTTTGTGC TGTACAAATA CAAGCTCCTG CCACGGTCTT GA
```

### Example 3

### Production of Truncated NCS

The *T. flavum* NCS sequence, courtesy of Peter Facchini, was that of the N-terminal MO truncation. To construct the full-length gene, the first 30 nucleotides (coding for 10 amino acids) were included in the forward primer sequence used for cloning the gene. For other variants, such as the A19 N-terminal truncation, the forward primer was designed to amplify the gene beginning at the $20^{th}$ amino acid and including an additional start codon if the new starting amino acid was not a methionine. To compare expression levels qualitatively, we cloned each variant into a yeast expression vector containing a V5 epitope tag (pYES2-NT/A, Invitrogen), transformed the plasmids into the wild-type yeast strain using the standard LiAc/SSD/PEG method (Gietz, R D and Woods, R A. *Methods in Enzymology*, Vol. 350, pp. 87-96, 2002), and performed Western blot analysis on the total protein lysates. This showed that the *T. flavum* NCSΔ10 was the most highly expressed in yeast, consistent with *E. coli* studies.

### Example 4

### Measurement of Dopamine Production

Yeast strains were constructed to produce dopamine from tyrosine. A high-copy—TRP plasmid containing TYDC2 and CYP2D6 both between the TEF1 promoter and CYC1 terminator was tested in various yeast strains. The standard LiAc/SSD/PEG method was used to transform the plasmid(s) into yeast. The CYP2D6 activity is enhanced as evidenced by an increase in dopamine production when the background strain is W(R), which overexpresses CPR1 from the chromosome. An additional increase in dopamine accumulation is observed when cells are co-transformed with a second plasmid expressing additional copies of CPR1 from the $tetO_7$ promoter. Alterations to the growth media have also been shown to enhance the activity of P450s in yeast (Jiang, H and Morgan, J A. Biotechnology and Bioengineering, Vol. 85, No 2, pp. 130-7). Media containing 3.4 g/L yeast nitrogen base, 5 g/L casein hydrolysate, and 20 g/L glucose was shown to improve dopamine production over standard SC media. For measurement of tyramine and dopamine accumulation, the growth media can be analyzed directly by LC-MS. Intracellular concentrations can be estimated by preparation of cell extracts. Briefly, cells are pelleted at 6000 rpm for 5 min at 4° C. and the supernatant carefully removed. Using a pipette, pellets of the cell paste are dropped into liquid nitrogen and a mortar and pestle used to homogenize the cells. Metabolites are extracted with methanol and solids removed by centrifugation; the liquid is passed through a syringe filter to remove any remaining debris. Appropriate dilutions are made prior to LC-MS analysis using 20 μL injection volume. Samples were run on an Agilent ZORBAX SB-Aq 3×250 mm, 5 μm column with 0.1% acetic acid as solvent A and methanol as solvent B. A gradient elution is used to separate the metabolites of interest: 0-10 min at 100% A, 10-30 min 0-90% B, 30-35 min 90-0% B, followed by a 5 min equilibration at 100% A. Tyrosine, tyramine, dopamine, and L-dopa elute within the first 10 min so that an isocratic elution may be used if analyzing only these and/or similar metabolites. Following LC separation, metabolites are injected into an Agilent 6320 ion trap MSD for detection. Extracted ion chromatograms are used to identify peaks for selected ions and compared to available standards in terms of elution time and MS fingerprint.



### Example 5

### Measurement of Norcoclaurine Production

Norcoclaurine was produced using both in vivo and in vitro methods. For in vitro experiments, protocols were based on published work (Samanani, N, Liscombe, D K, and Facchini, P. *The Plant Journal*, Vol. 40, pp. 302-313). Both *E. coli* and yeast cells expressing NCS variants were lysed with B-PER or Y-PER (Pierce), respectively, and total protein extracts were used in the assay. In vitro reactions were analyzed by LC-MS. Samples were run on an Agilent ZORBAX SB-Aq 3×250 mm, 5 μm column with 0.1% acetic acid as solvent A and methanol as solvent B. A gradient elution is used to separate the metabolites of interest: 0-10 min at 100% A, 10-30 min 0-90% B, 30-35 min 90-0% B, followed by a 5 min equilibration at 100% A. Following LC separation, metabolites are injected into an Agilent 6320 ion trap MSD for detection. Norcoclaurine elutes at 21.2 min using this method. Without a commercially available standard, norcoclaurine is confirmed by its characteristic fragmentation pattern. With the ion trap set to perform MS/MS in the 272 ion, the major fragments of the parent ion of m/z=107 (benzyl) and m/z=161 (isoquinoline) were identified. For in vivo experiments, yeast cells expressing NCS were supplemented with dopamine (between 10 μM and 1 mM) and 4-HPA (custom synthesized from Biosynthesis, concentration undetermined). The above method was used to analyze the growth media directly to detect extracellular norcoclaurine accumulation.

### Example 6

### Production and Measurement of Reticuline and its Intermediates

For production of reticuline from the substrate norlaudanosoline (or laudanosoline), yeast cells were transformed with plasmids expressing various combinations of 6OMT, CNMT, and 4'OMT coding sequences using the standard LiAc/SSD/PEG method. Yeast cells were grown in SC media lacking uracil and tryptophan for plasmid maintenance. The growth media (SC-URA/-TRP) was supplemented with norlaudanosoline at concentrations between 1-5 mM from a 10 or 20 mM stock solution in water. Cells were grown in test tubes at 30° C. with shaking at 200 rpm; volumes ranged from 1-10 mL and time points were from 8 hrs up to 1 week following addition of substrate. Cells (or an aliquot of culture) were pelleted and the supernatant analyzed directly by LC-MS. Samples were run on an Agilent ZORBAX SB-Aq 3×250 mm, 5 column with 0.1% acetic acid as solvent A and methanol as solvent B. A gradient elution is used to separate the metabolites of interest: 0-10 min at 100% A, 10-30 min 0-90% B, 30-35 min 90-0% B, followed by a 5 min equilibration at 100% A. Following LC separation, metabolites are injected into all Agilent 6320 ion trap MSD for detection. Reticuline elutes at 23.6 min with this method and the correct structure of this metabolite is confirmed by performing MS/MS on the 330 ion to produce the fragments m/z=136 and m/z=192. Based on the results from plasmid-based expression, the *P. somniferum* 6OMT and CNMT were selected with either the *P. somniferum* or *T. flavum* 4'OMT as the best enzyme combinations, and these sequences were integrated into the chromosome using homologous recombination. In addition, strains were constructed to test each enzyme individually, typically using a single high-copy plasmid with the TEF promoter driving expression of the coding sequence. For the 6OMT activity, the correct product, 6-O-methyl norlaudanosoline, was detected by LC-MS when norlaudanosoline was present in the growth media; in vitro assays based on published protocols and using yeast lysates were also used to confirm this activity (Ounaroon, A et. Al. *The Plant Journal*, Vol. 36, pp. 808-19). Yeast cells expressing the CNMT enzyme converted 6,7-dimethyl-1,2,3,4-tetrahydroisoquinoline present at 1 mM in the growth media to the correct N-methylated product in vivo. Yeast cells expressing the 4'OMT enzyme methylated the substrates norlaudanosoline and laudanosoline in vivo. The correct location of the methyl group addition to each substrate is confirmed by performing MS/MS on the selected ion in all cases.

## Example 7

### Production and Measurement of Downstream Metabolites of Reticuline

For production of metabolites beyond reticuline, yeast strains with chromosomal integrations of 6OMT, CNMT, and 4'OMT were used when possible. These host cells contained no selection markers, allowing for additional coding sequences to be introduced on plasmids. For production of scoulerine, a plasmid expressing BBE was transformed into reticuline-producing strain(s) using the standard LiAc/SSD/PEG method. For production of tetrahydrocolumbamine, plasmids expressing BBE and S9OMT were cotransformed. For production of canadine, plasmids expressing BBE, S9OMT, CYP719A, and ATR1 were contransformed. Construction of a yeast strain to stably express ATR1 along with the reticuline-producing enzymes and transformed with BBE, S9OMT, and CYP719A plasmids showed an increase in CYP719A activity (compared to plasmid-based expression of ATR1) demonstrated by increased conversion of substrate to canadine. Metabolites were detected in the growth media when supplemented with 1 mM or greater norlaudanosoline or laudanosoline. Samples were run on an Agilent ZORBAX SB-Aq 3×250 mm, 5 μm column with 0.1% acetic acid as solvent A and methanol as solvent B. A gradient elution is used to separate the metabolites of interest: 0-10 min at 100% A, 10-30 min 0-90% B, 30-35 min 90-0% B, followed by a 5 min equilibration at 100% A. Following LC separation, metabolites are injected into an Agilent 6320 ion trap MSD for detection. For each metabolite in the pathway, MS/MS was performed and the spectra compared. Based on the patterns observed, it can be confirmed that the peak identified as canadine, for example, has the same molecular structure as its precursor, tetrahydrocolumbamine. For production of salutaridine, the yeast strain stably expressing 6OMT, CNMT, 4'OMT, and ATR1 was transformed with a plasmid expressing CYP2D6. When the growth media was supplemented with norlaudanosoline or laudanosoline, salutaridine was detected by LC-MS. The elution time of salutaridine is identical to that of scoulerine as expected although its fragmentation pattern, particularly the 165 ion, indicates that the structure is in the correct (R) conformation based on the reported fragmentation pattern of salutaridinol.

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agtttgtagg tggatctggt caagtgagcg aacggataat ggacctcctc ggagaccaag    720

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ctgatcgact tgctaagcta cataaggaaa taaggaagaa gaaaatctgt gagctctatg   1140

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tgtacaaata caagctcctg ccacggtctt ga                                 1592
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What is claimed is:

1. A method of preparing a metabolite of tyrosine that is a benzylisoquinoline alkaloid product, the method comprising:

a) culturing an engineered non-plant cell under conditions suitable for protein production, said engineered non-plant cell comprising three heterologous coding sequences, wherein the three heterologous coding sequences encode a first, second, and third enzyme, respectively, that are involved in a metabolic pathway that converts the tyrosine into the benzylisoquinoline alkaloid product, wherein the first, second, and third enzymes are operably connected along the metabolic pathway;

b) optionally adding tyrosine to the cell culture; and

c) recovering the benzylisoquinoline alkaloid product from the cell culture,

wherein the benzylisoquinoline alkaloid product is selected from the group consisting of a norcoclaurine, coclaurine, N-methylcoclaurine, 3'-hydroxy-N-methylcoclaurine, reticuline, 6-O-methyl-norlaudanosoline, 6-O-methyl-laudanosoline, laudanine, scoulerine, tetrahydrocolumbamine, canadine, salutaridine, salutaridinol, salutaridinol-7-O-acetate, and thebaine, and

wherein each of the first, second, and third enzymes involved in the metabolic pathway that produces the benzylisoquinoline alkaloid product is selected from the group consisting of L-tyrosine/dopa decarboxylase 1, L-tyrosine/dopa decarboxylase 2, Cytochrome P450 2D6, NADPH p450 reductase, Polyphenyloxidase, Tyrosine hydroxylase, GTPcyclohydrolase I, Monoamine oxidase A, Tyramine oxidase, Aromatic amino acid transaminase, Phenylpyruvate decarboxylase, Norcoclaurine synthase, Norcoclaurine 6-O-methyltransferase, Coclaurine-N-methyltransferase, Cytochrome P450 80B1, 4-O-methyltransferase, Berberine bridge enzyme, Reticuline 7-O-methyltransferase, Scoulerine 9-O-methyltransferase, Canadine synthase, Salutaridine reductase, Salutaridinol 7-O-acetyltransferase, Codeine reductase, and Berbamunine synthase.

2. The method of claim 1, wherein the benzylisoquinoline alkaloid product is selected from the group consisting of norcoclaurine, coclaurine, N-methylcoclaurine, 3'-hydroxy-N-methylcoclaurine, reticuline, 6-O-methyl-laudanosoline, laudanine, scoulerine, tetrahydrocolumbamine, canadine, salutaridine, salutaridinol, salutaridinol-7-O-acetate, and thebaine.

3. The method of claim 1, wherein the engineered non-plant cell is selected from the group consisting of microbial cells, insect cells, mammalian cells, bacterial cells, and yeast cells.

4. The method of claim 1, wherein the engineered non-plant cell is cultured under in vitro conditions.

5. The method of claim 1, wherein the engineered non-plant cell is cultured under in vivo conditions.

6. The method of claim 1, wherein the engineered non-plant cell is cultured with a compound selected from the group consisting of tyrosine, tyramine, dopamine, 4-hydroxyphenylacetaldehyde, 4-hydroxyphenylpyruvate, norcoclaurine, coclaurine, N-methylcoclaurine, 3'-hydroxy-N-methylcoclaurine, reticuline, scoulerine, tetrahydrocolumbamine, laudanosoline, and norlaudanosoline.

7. The method of claim 1, wherein the engineered non-plant cell is cultured with tyrosine, and wherein the recovered benzylisoquinoline alkaloid product is norcoclaurine.

8. The method of claim 1, wherein the engineered non-plant cell comprises at least one of L-tyrosine/dopa decarboxylase 1, L-tyrosine/dopa decarboxylase 2, Norcoclaurine synthase, and Cytochrome P450 2D6.

9. The method of claim 1, wherein the engineered non-plant cell is cultured with tyrosine, and wherein the recovered benzylisoquinoline alkaloid product is reticuline.

10. The method of claim 9, wherein the engineered non-plant cell comprises at least one of L-tyrosine/dopa decarboxylase 1, L-tyrosine/dopa decarboxylase 2, Cytochrome P450 2D6, Monoamine oxidase A, Norcoclaurine synthase, Norcoclaurine 6-O-methyltransferase, Coclaurine-N-methyltransferase, Cytochrome P450 80B1, and 4-O-methyltransferase.

11. The method of claim 1, wherein the engineered non-plant cell is cultured with tyrosine, wherein the engineered non-plant cell comprises at least one of L-tyrosine/dopa decarboxylase 1, L-tyrosine/dopa decarboxylase 2, Cytochrome P450 2D6, Monoamine oxidase A, Norcoclaurine synthase, Norcoclaurine 6-O-methyltransferase, Coclaurine-N-methyltransferase, Cytochrome P450 80B1, 4-O-methyltransferase, and Berberine bridge enzyme, and wherein the recovered benzylisoquinoline alkaloid product is scoulerine.

12. The method of claim 1, wherein the engineered non-plant cell is cultured with norlaudanosoline, wherein the engineered non-plant cell comprises at least one of Norcoclaurine 6-O-methyltransferase, Coclaurine-N-methyltransferase, and 4-O-methyltransferase, and wherein the recovered benzylisoquinoline alkaloid product is selected from the group consisting of 6-O-methyl norlaudanosoline, 3'-hydroxy-N-methylcoclaurine, and reticuline.

13. The method of claim 1, wherein the engineered non-plant cell is cultured with reticuline, wherein the engineered non-plant cell comprises at least one of Berberine bridge enzyme, Scoulerine 9-O-methyltransferase, and Canadine synthase, and wherein the recovered benzylisoquinoline alkaloid product is selected from the group consisting of scoulerine, tetrahydrocolumbamine, and canadine.

14. The method of claim 1, wherein the engineered non-plant cell is cultured with reticuline, wherein the engineered non-plant cell comprises at least one of Cytochrome P450 2D6, Salutaridine reductase, and Salutaridinol 7-O-acetyltransferase, and wherein the recovered benzylisoquinoline alkaloid product is selected from the group consisting of salutaridine, salutaridinol, salutarinidol-7-O-acetate, and thebaine.

15. The method of claim 1, wherein the engineered non-plant cell is cultured with norcoclaurine, wherein the engi-

neered non-plant cell comprises at least one of Norcoclaurine 6-O-methyltransferase, Coclaurine-N-methyltransferase, Cytochrome P450 80B1, 4-O-methyltransferase, Berberine bridge enzyme, Scoulerine 9-O-methyltransferase, and Canadine synthase, and wherein the recovered benzylisoquinoline alkaloid product is selected from the group consisting of coclaurine, scoulerine, reticuline, 3'-hydroxy-N-methylcoclaurine, N-methylcoclaurine, tetrahydrocolumbamine, and canadine.

**16**. The method of claim **1**, wherein the engineered non-plant cell is cultured with norcoclaurine, wherein the engineered non-plant cell comprises at least one of Norcoclaurine 6-O-methyltransferase, Coclaurine-N-methyltransferase, Cytochrome P450 80B1, 4-O-methyltransferase, and Cytochrome P450 2D6, Salutaridine reductase, and Salutaridinol 7-O-acetyltransferase, and wherein the recovered benzylisoquinoline alkaloid product is thebaine.

**17**. The method of claim **1**, wherein the engineered non-plant cell is cultured with a second non-plant cell, wherein the second non-plant cell produces at least one of tyrosine, tyramine, dopamine, 4-hydroxyphenylacetaldehyde, 4-hydroxyphenylpyruvate, norcoclaurine, coclaurine, N-methylcoclaurine, 3'-hydroxy-N-methylcoclaurine, reticuline, scoulerine, tetrahydrocolumbamine, laudanosoline, and norlaudanosoline.

**18**. The method of claim **1**, wherein recovering the benzylisoquinoline alkaloid product from the cell culture comprises separating the benzylisoquinoline alkaloid product from cellular material to provide a product stream having the benzylisoquinoline alkaloid product.

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